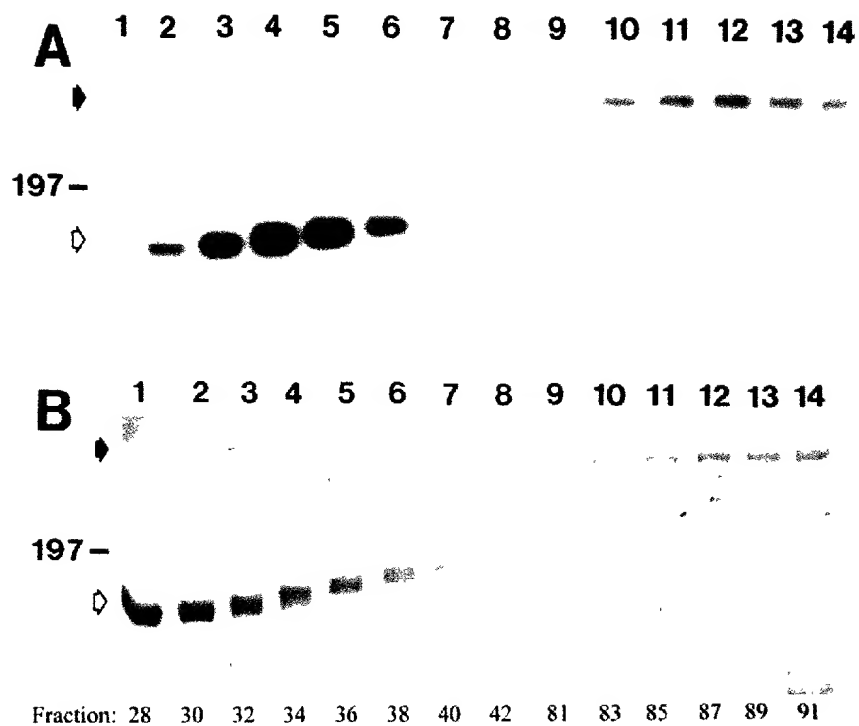
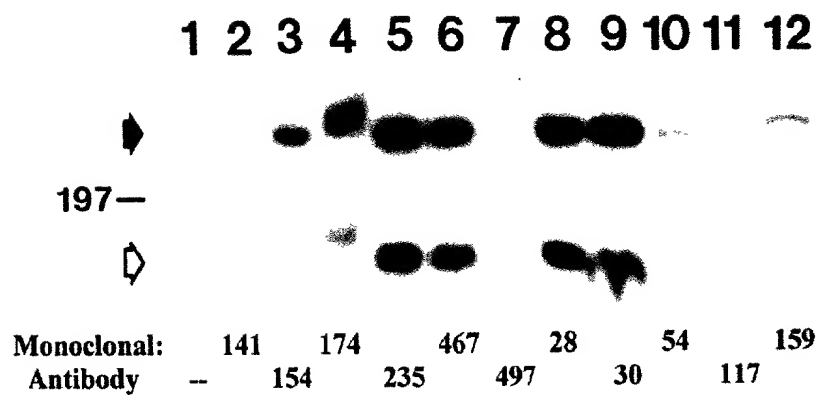


#6

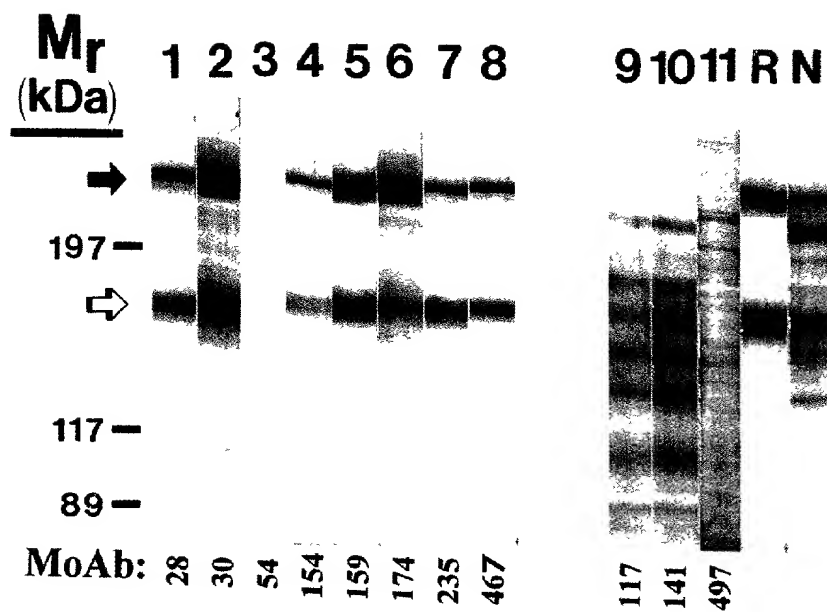
# Figure 1



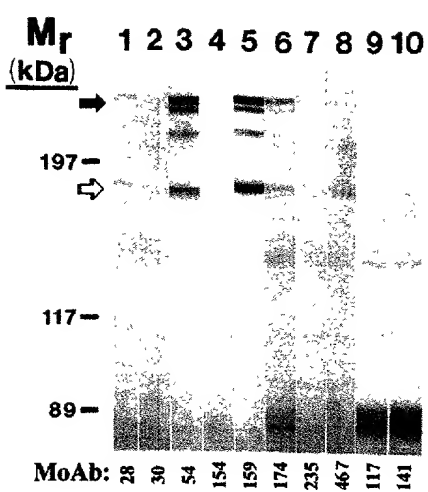
# Figure 2



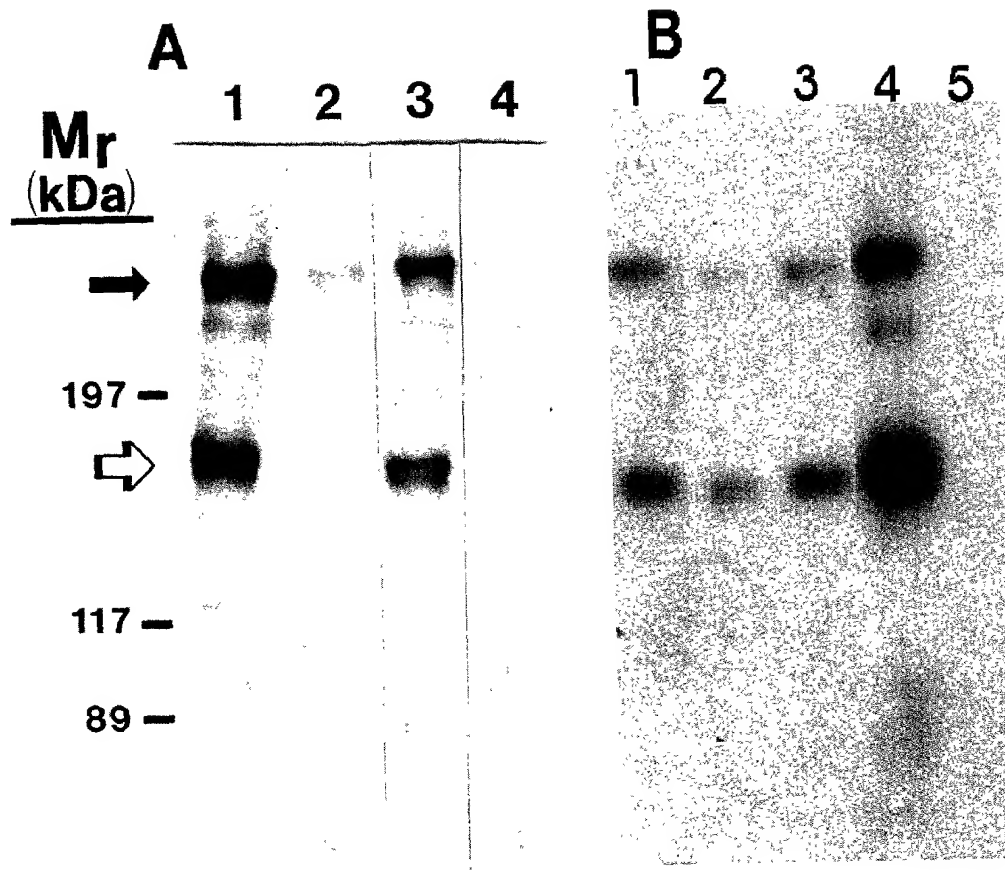
# Figure 3



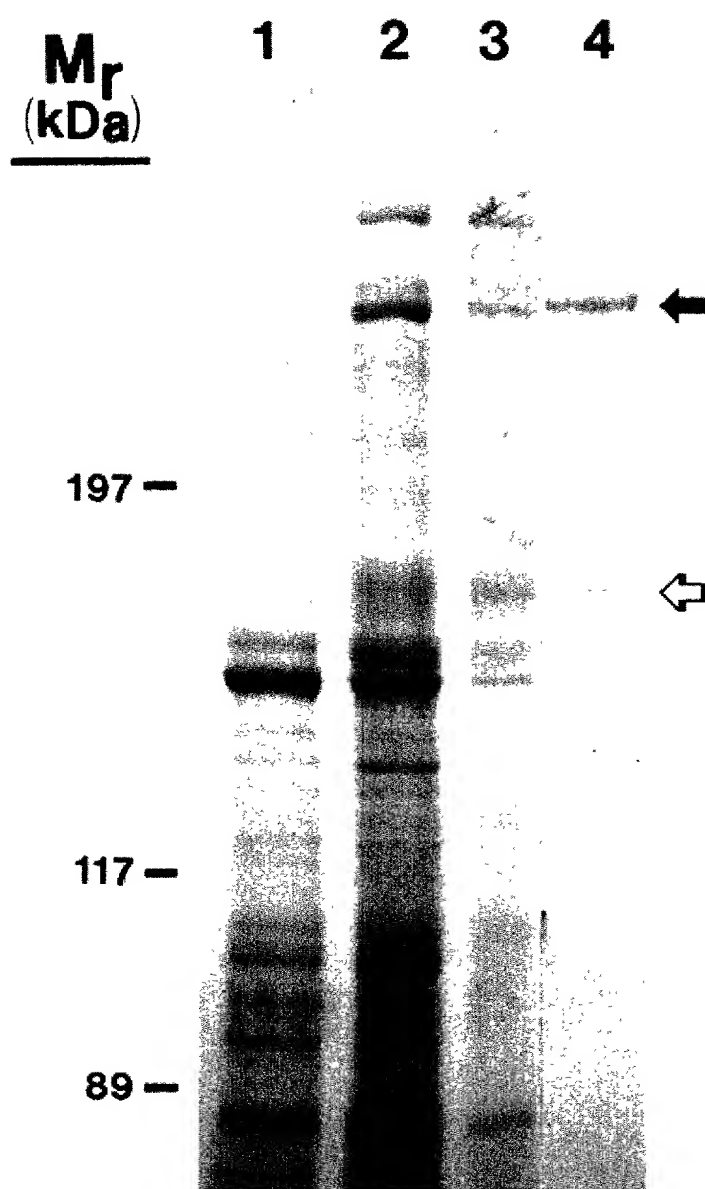
# Figure 4



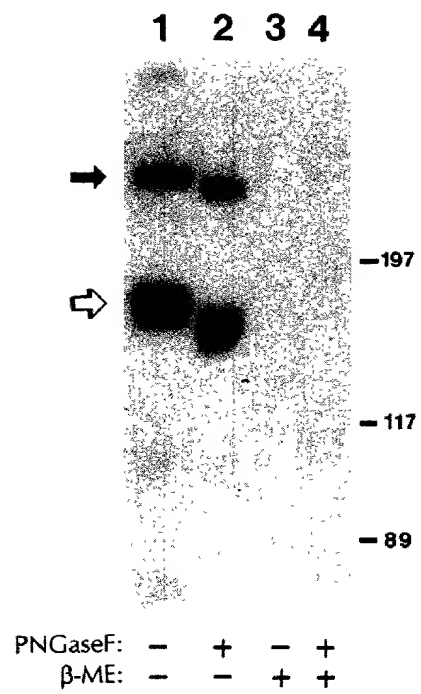
# Figure 5



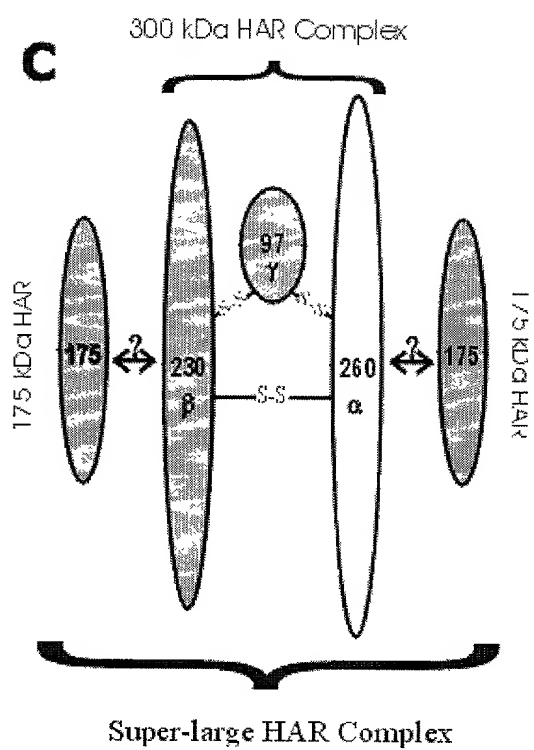
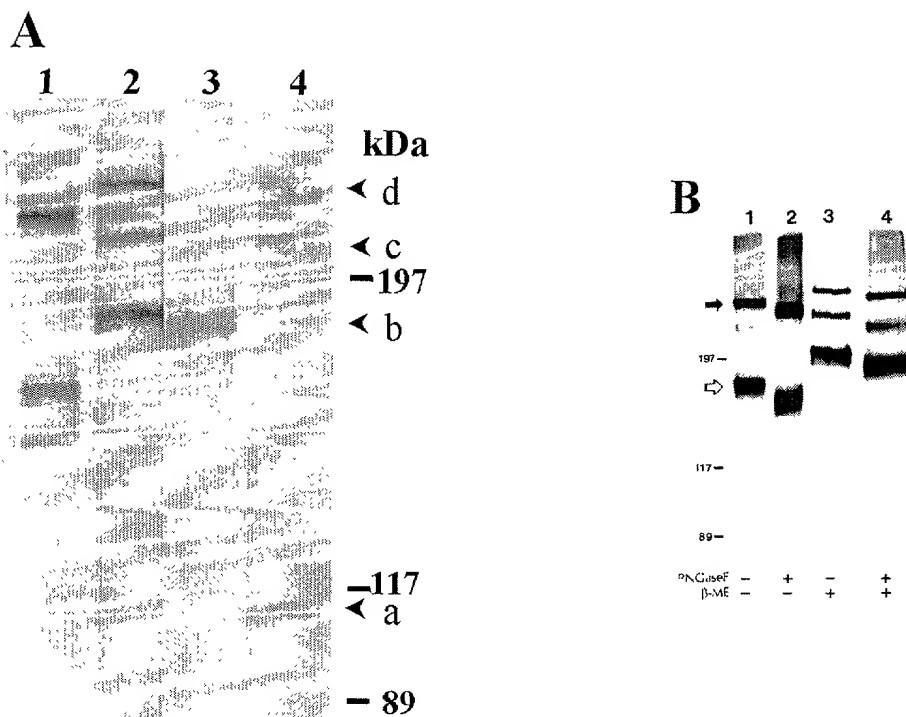
# Figure 6



# Figure 7



# Figure 8





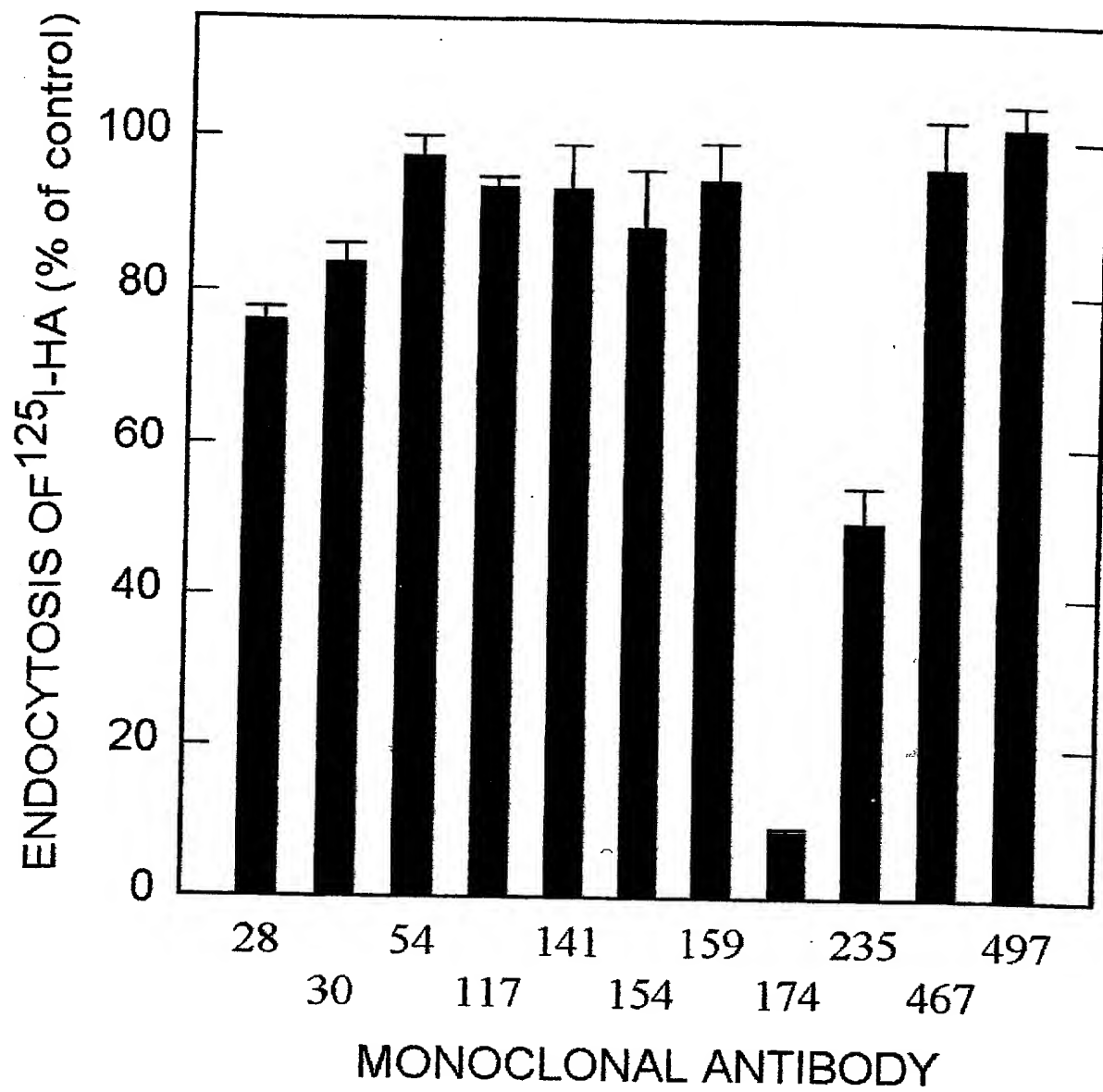


Figure 9

# Figure 10

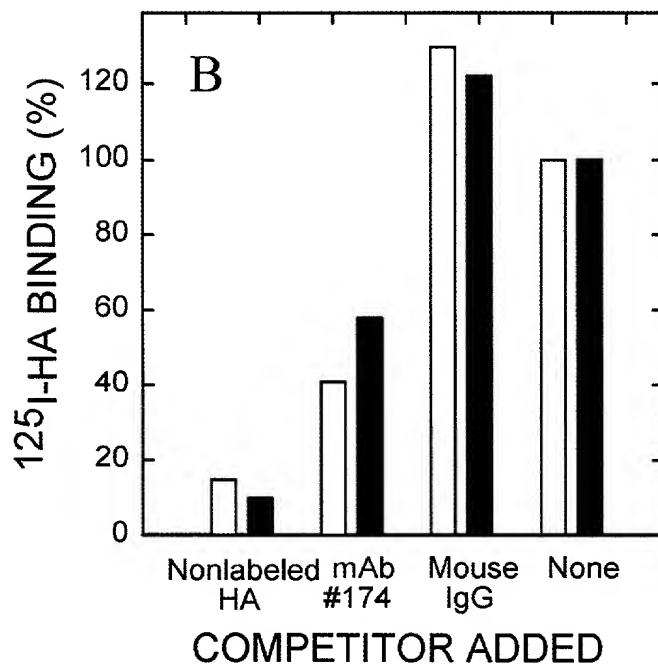
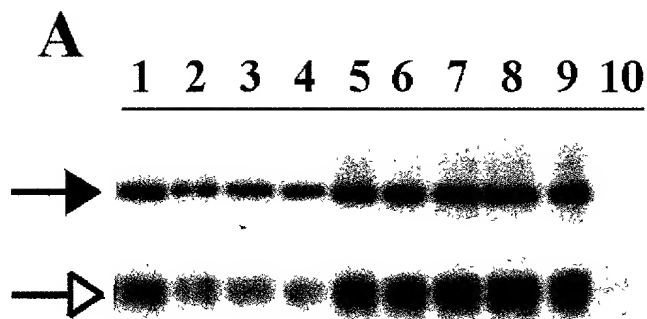


Figure 11

### Antibody Inhibition of HA Endocytosis by HARE in LECs

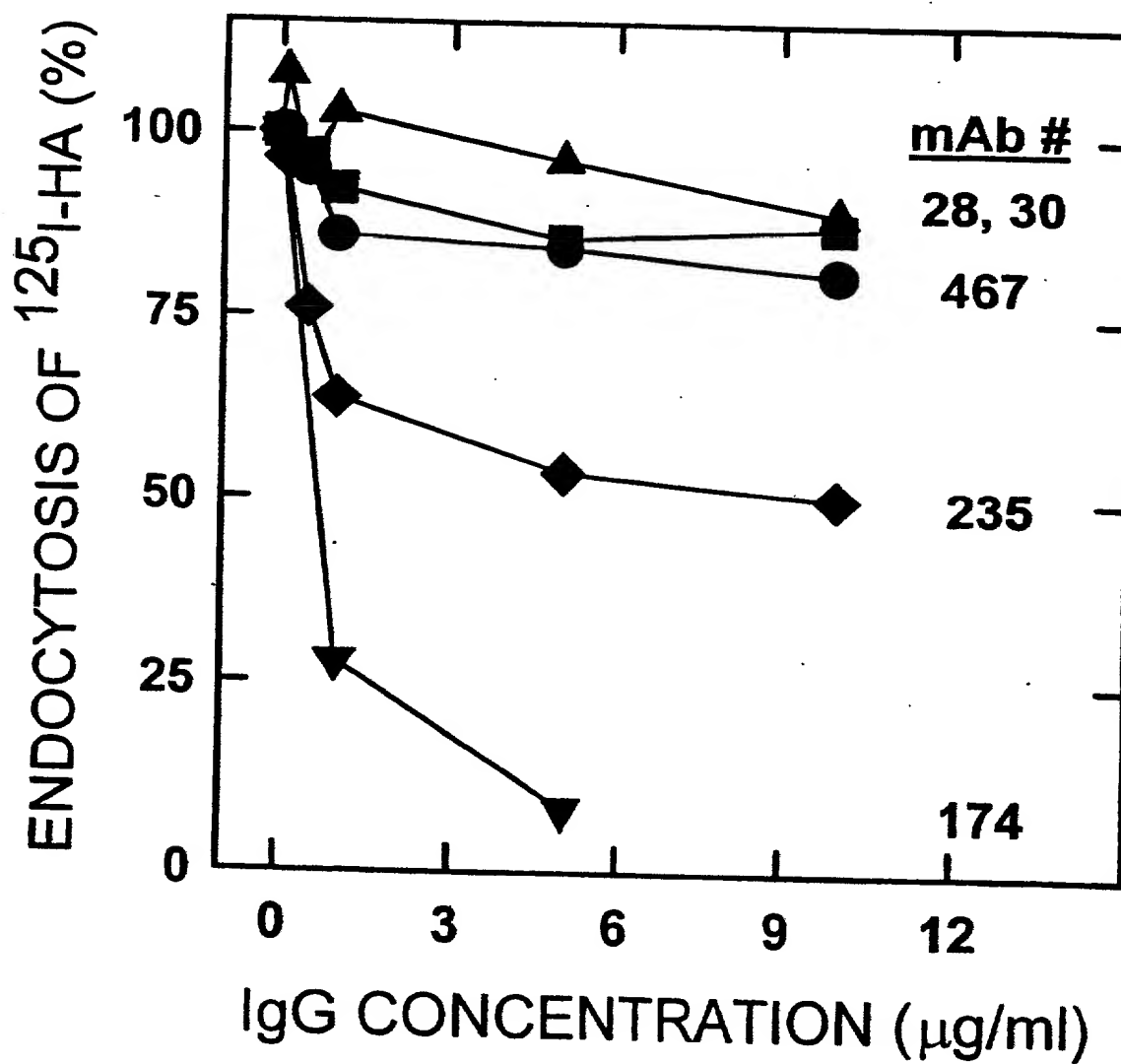
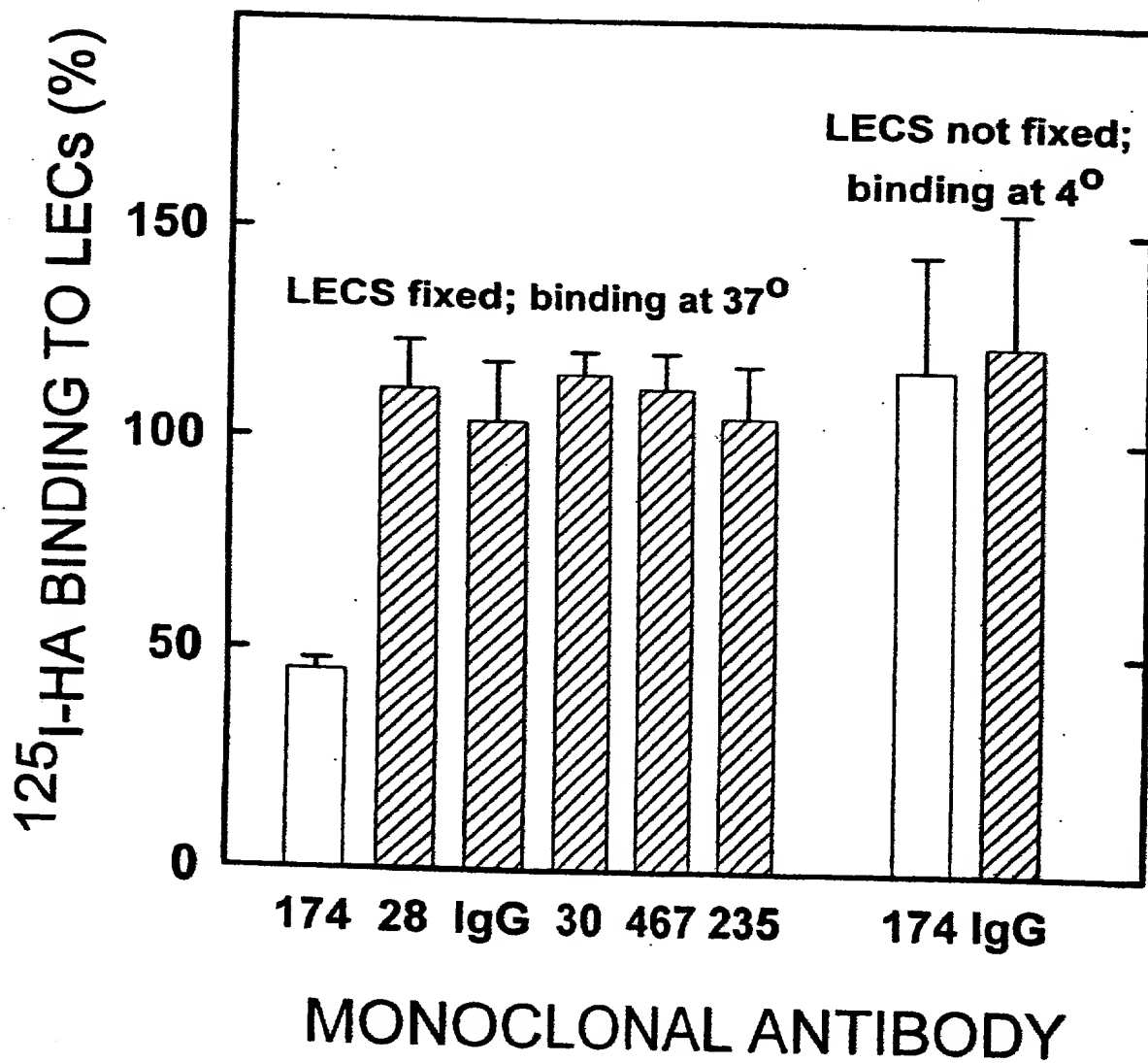


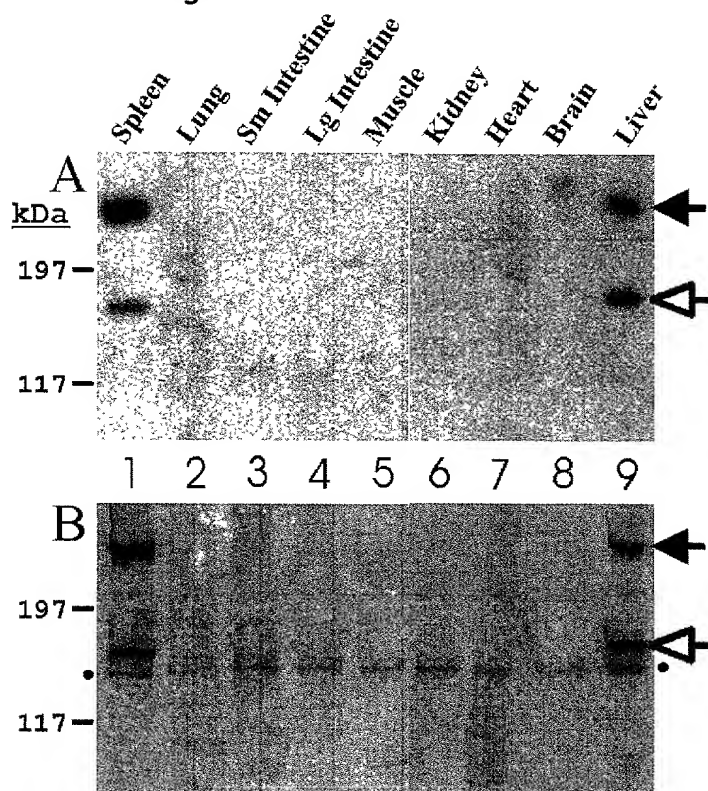
Figure 12

**Antibody Inhibition of HA Binding to HARE  
on LECs is Temperature Dependent**

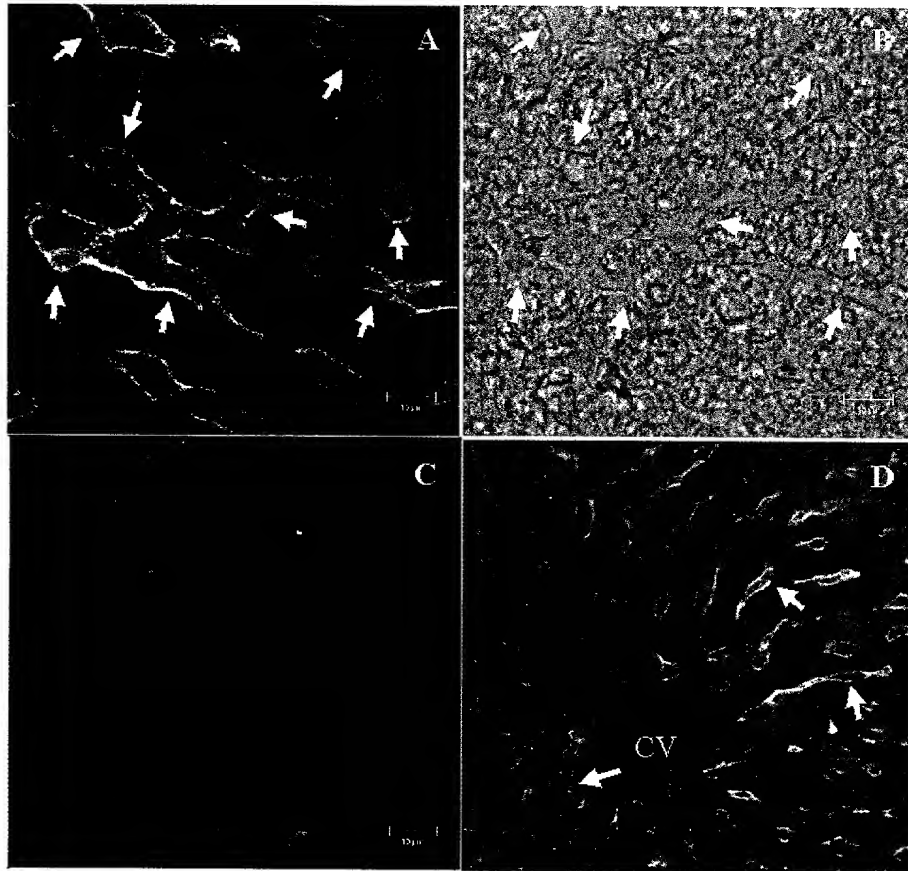


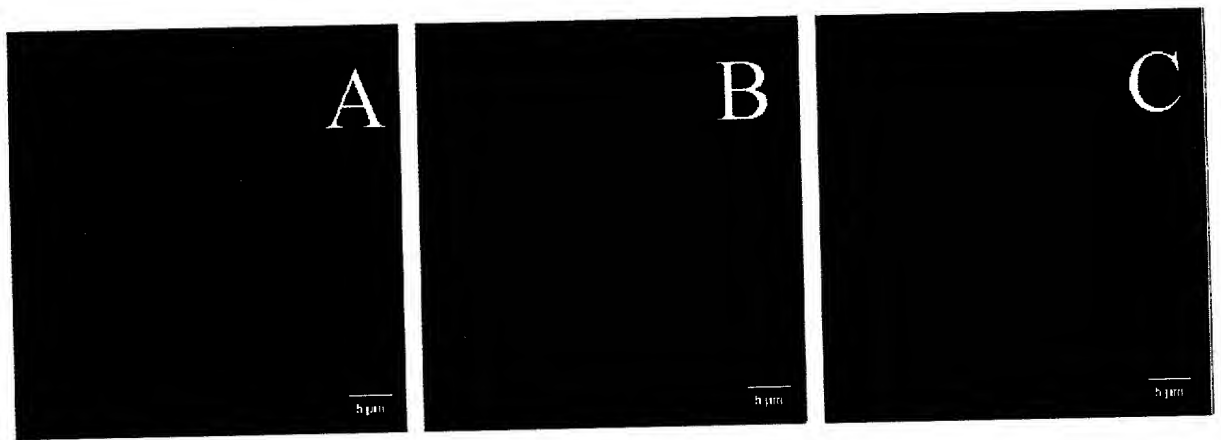
# Figure 13

Figure 13



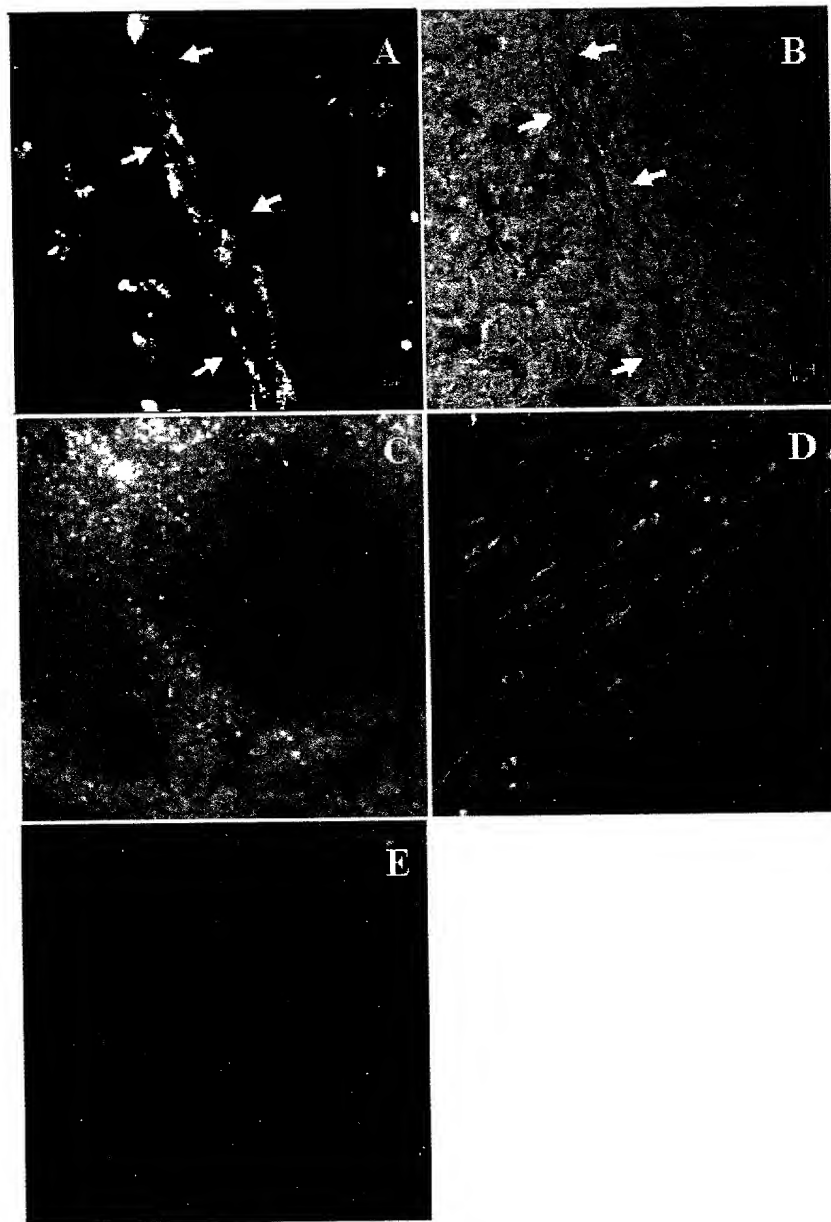
# Figure 14



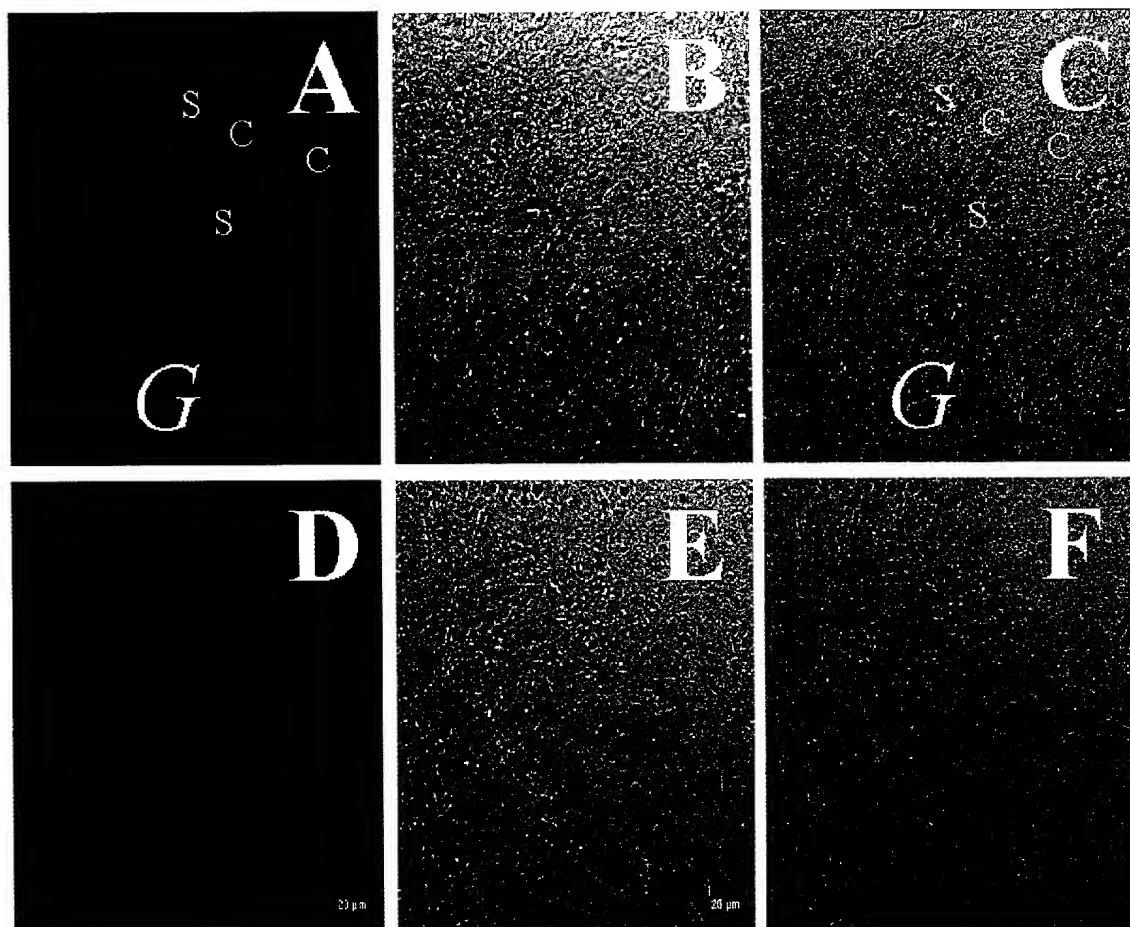


**Figure 15**

# Figure 16





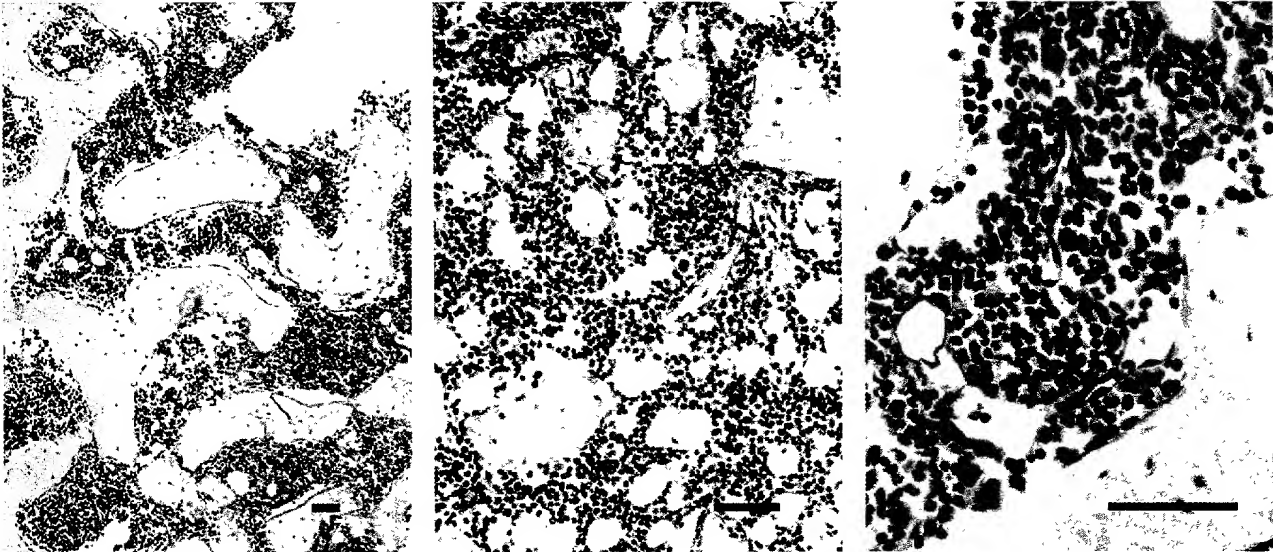


**Figure 17**

Figure 18

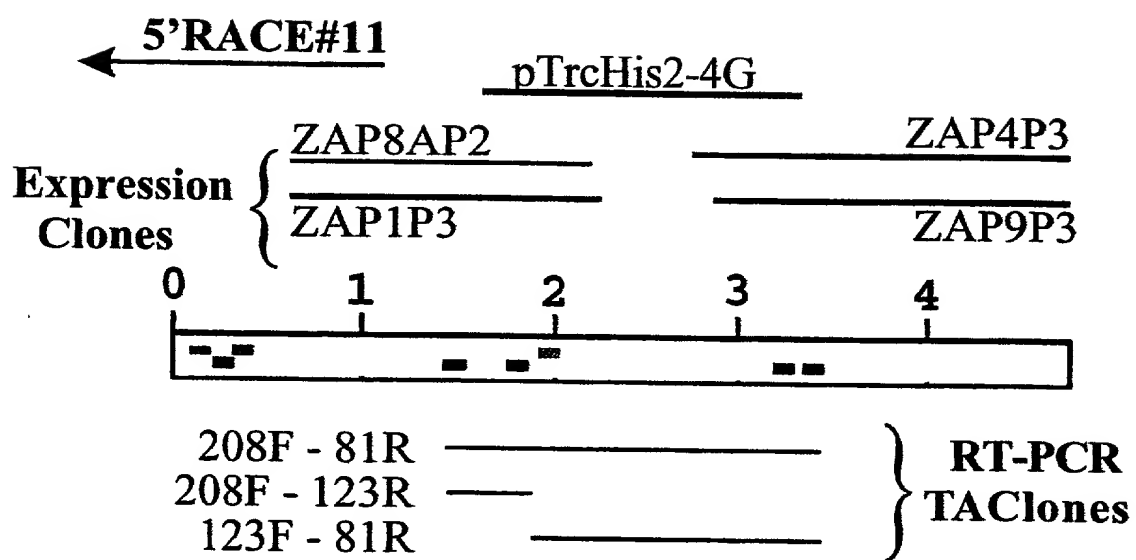
**Immunolocalization of HARE  
in Bone Marrow**

**Control**

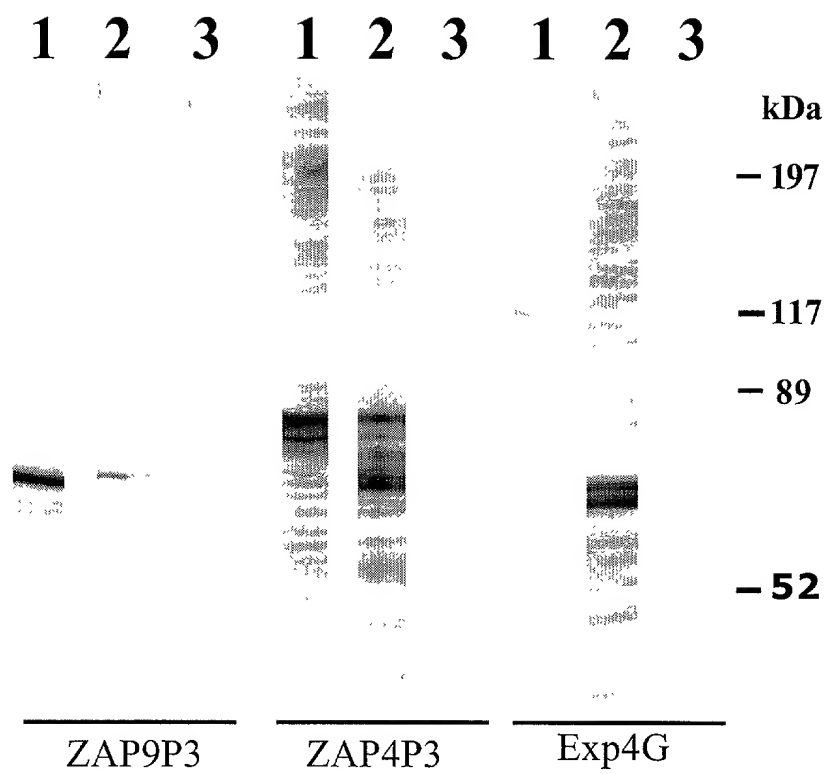


**Bars = 50 um**

Figure 19



**Figure 20**



**Figure 21**

[illegible]

Figure 22

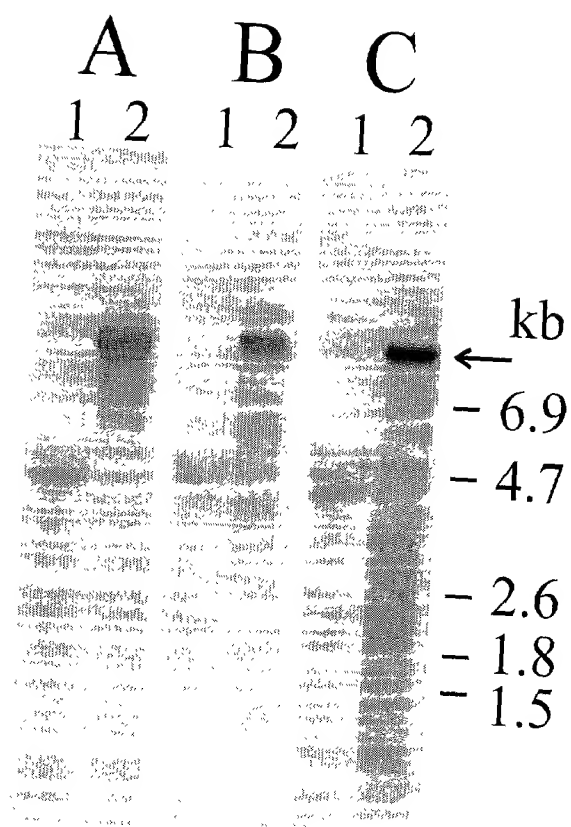


Figure 23

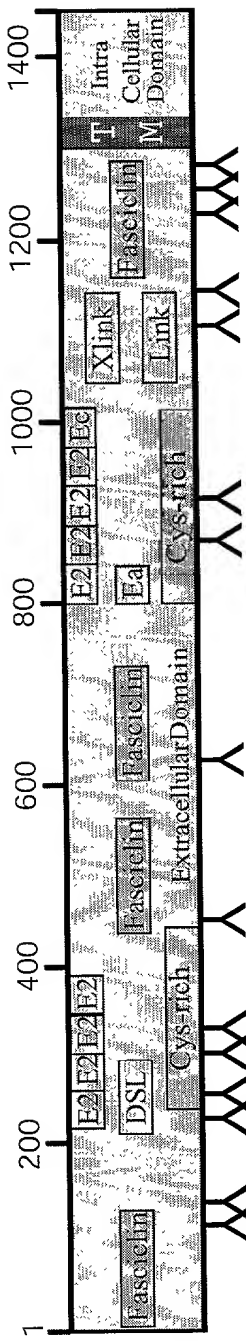






Figure 25

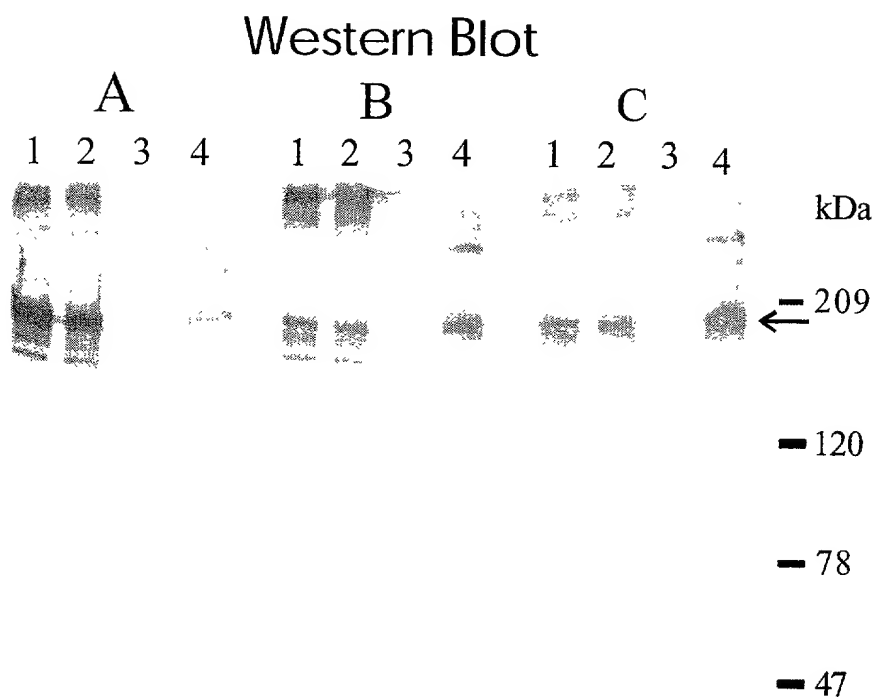
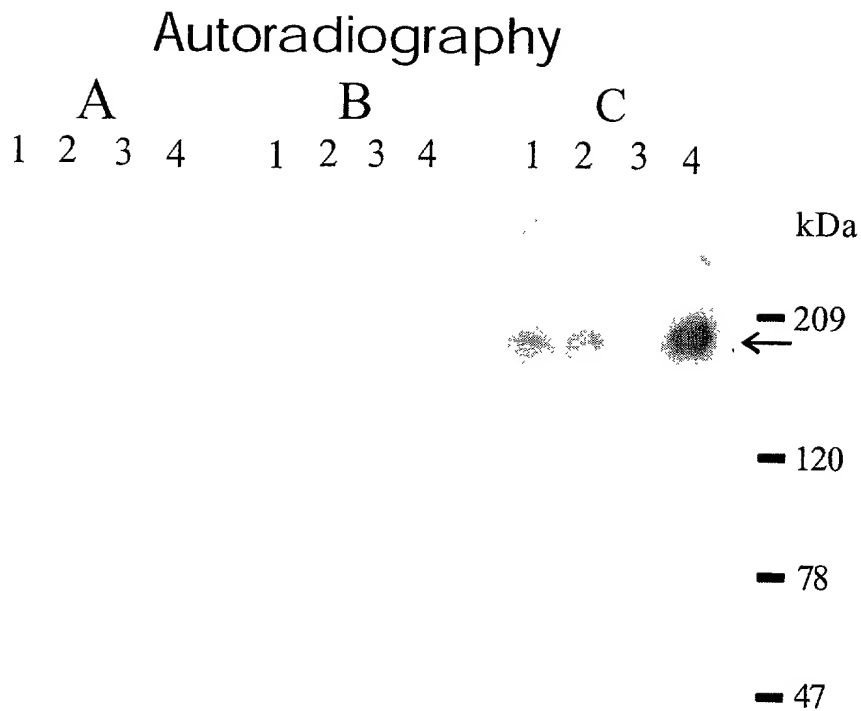


Figure 26

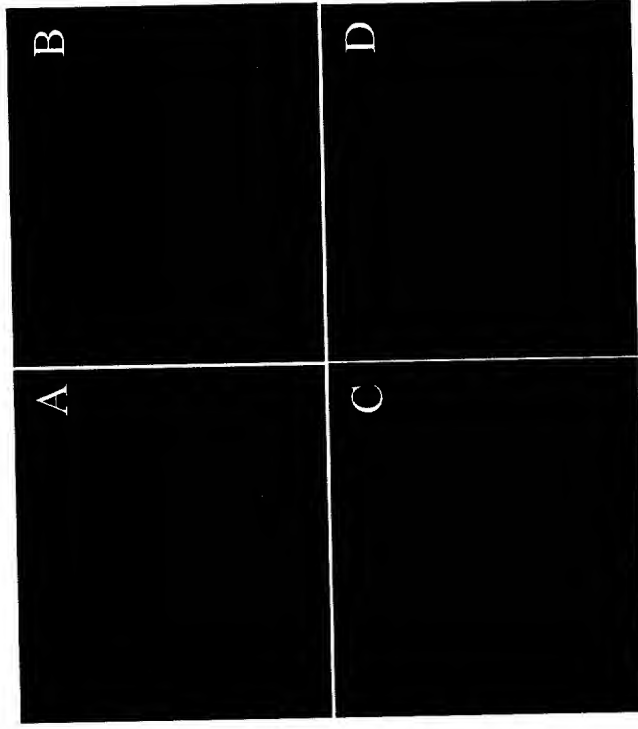


Figure 27A

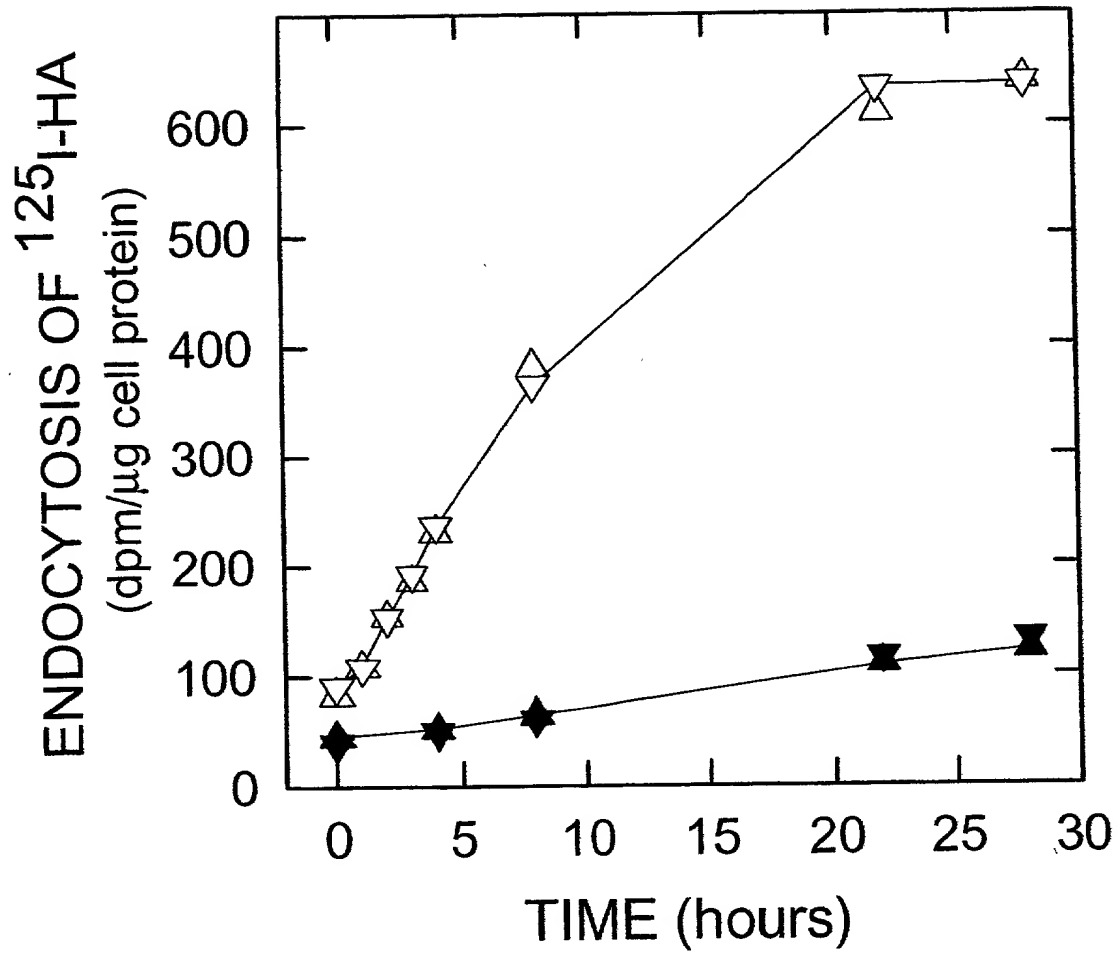


Figure 27B

**Degradation of internalized HA by transfected SK-Hep1 cell lines expressing the 175-kDa HARE**

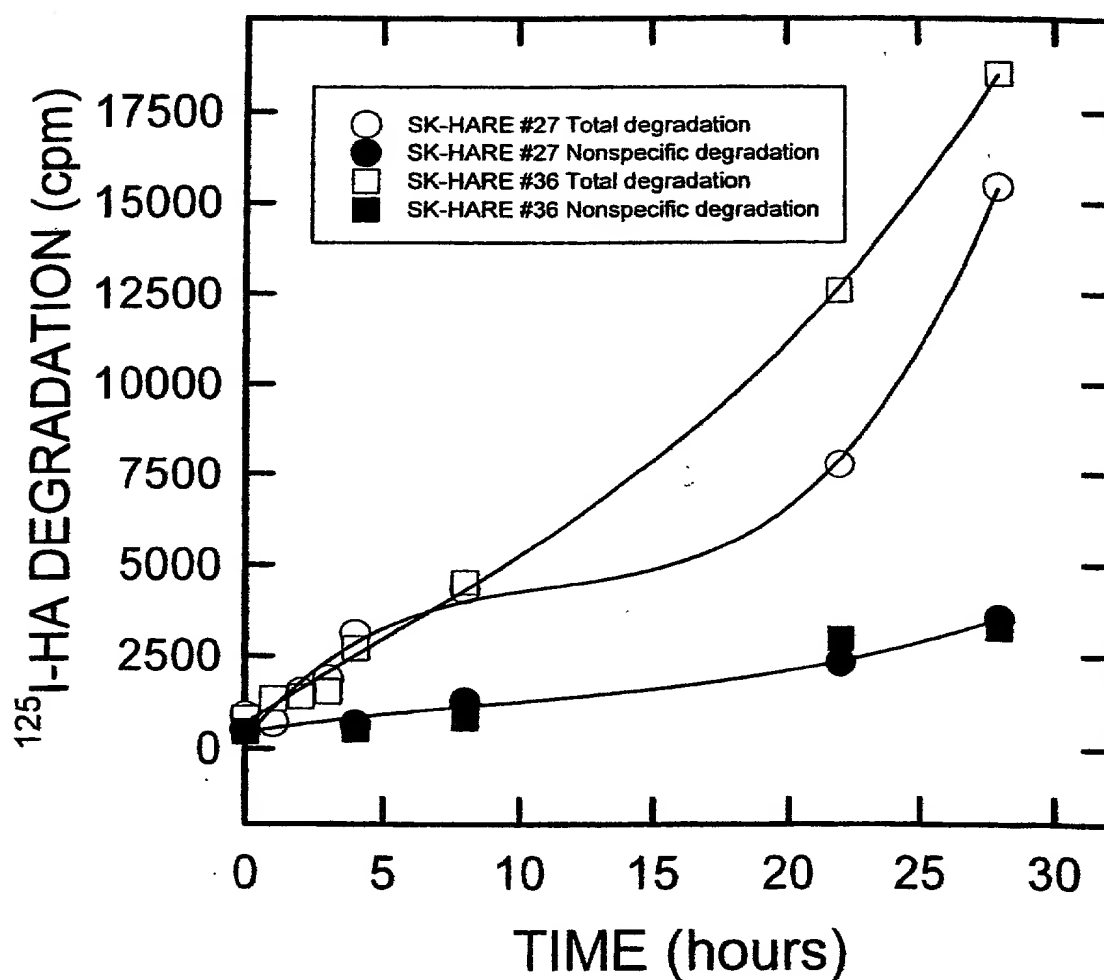


Figure 27C

**Hyperosmolarity inhibits HA endocytosis mediated by HARE in transfected SK-Hep1 cells**

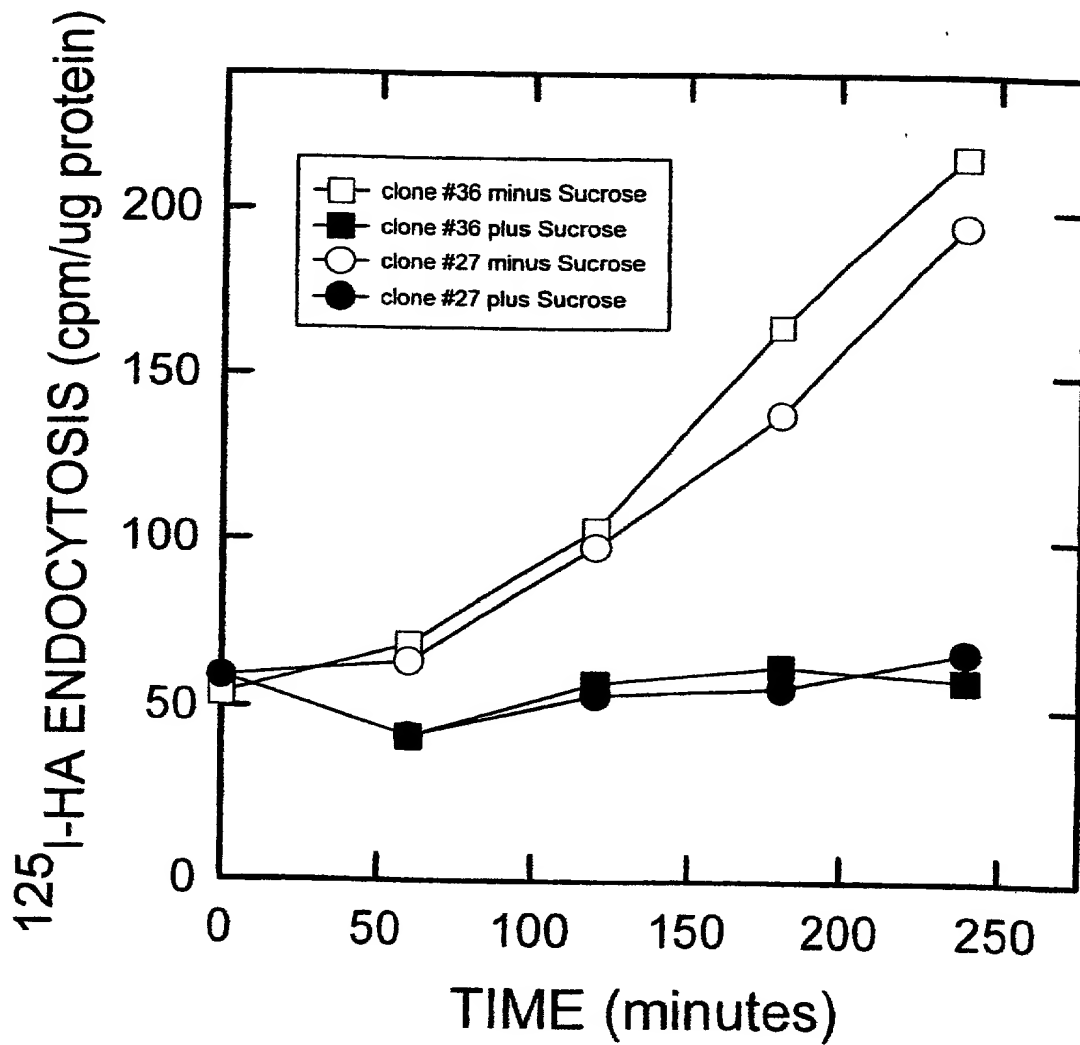


Figure 27D

**Specific monoclonal antibodies against HARE  
inhibit HA endocytosis in SK-Hep1  
transfectants expressing the 175-kDa HARE**

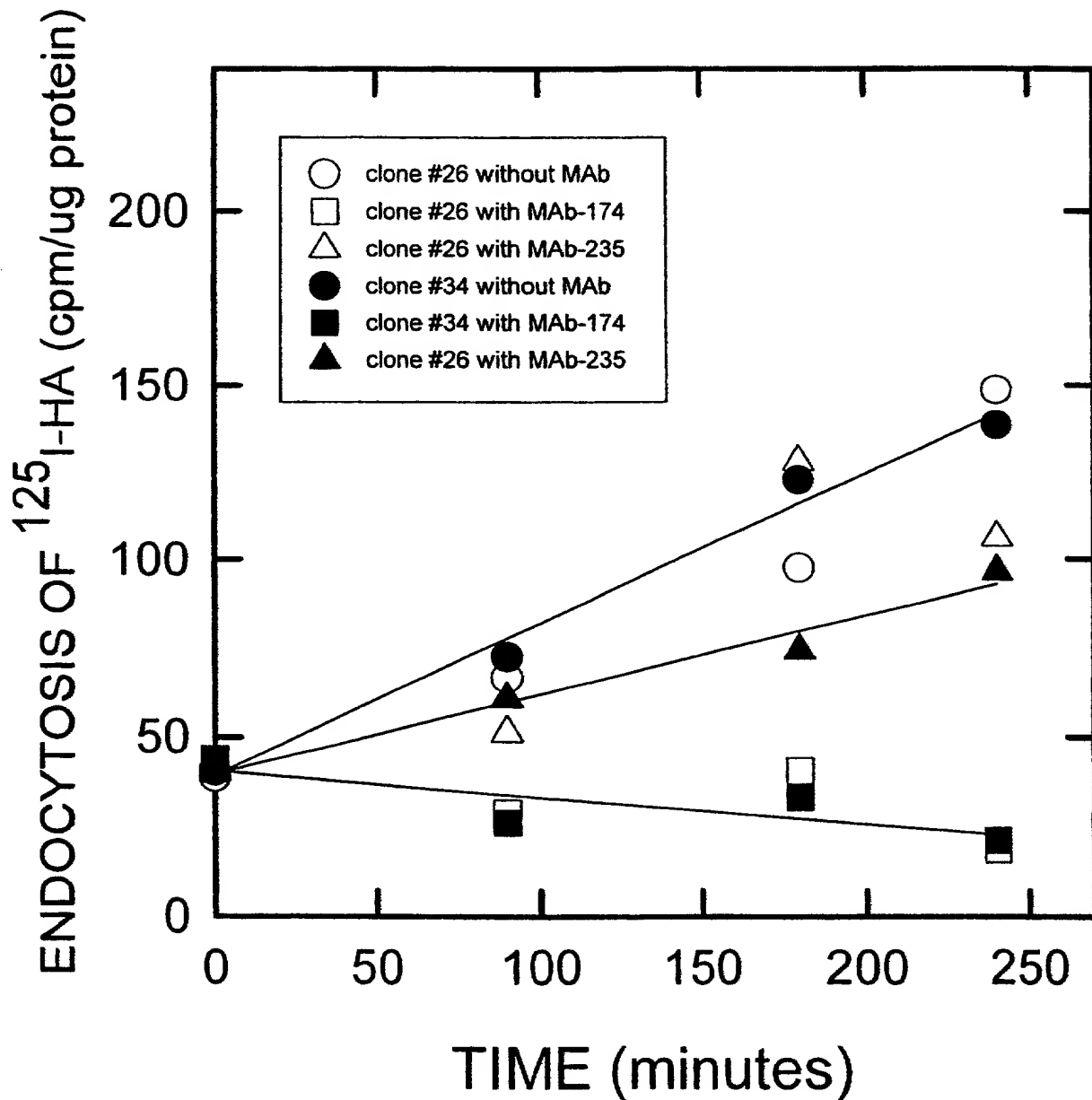


Figure 28

175SHARE 1 -----SLPS LLTRLQMPD YSI PRGYI IH YNLASAI ESA DAYTVFVPPN EAREN YIREK KATSLKED IL RYHVVGLBKL LKNDLHNGHM RETMLGPSYL  
CAB61827 1111 LHILSQVLLP PRGDVPGQG LLQQLDLVA FSLPRELLQH HGUVQI EAA TAYTIFVPPN RSLA ---QG NSSHLADATV RHHVVLGEL SMETLRKGGH RNSLLGPAHW  
BAA13377 754 LHILSQVLLP PRGDVPGQG LLQQLDLV-A FSLPRELLQH HGUVQI EAA TAYTIFVPPN RSLA ---QG NSSHLADATV RHHVVLGEL SMETLRKGGH RNSLLGPAHW

175SHARE 95 LAFPLYRQQL YVNEAP INYT NVATDKGVH GLEKVLBCK NR ENNDTII VGRGSKRSO QAPFLETKP LRETRK-ITV SIYPMGKRSV FIGQPCQVR TITRAVLA  
CAB61827 1218 IVFYNHSSQP EVNHVPLBGP MLEAPGRSLI GLSGVLTVGS SR LSHSHEA LREKVNITR RFRITQGFOL QDTPRKSIVY RSGGFSFR-- --G SYTAK KIQVPLCPG  
BAA13377 861 IVFYNHSSQP EVNHVPLBGP MLEAPGRSLI GLSGVLTVGS SR LSHSHEA LREKVNITR RFRITQGFOL QDTPRKSIVY RSGGFSFR-- --G SYTAK KIQVPLCPG

175SHARE 204 SLAHNAKPAE GEVK-MALG TASVMDGVNG TGTI-GLGF NGTANETIE GKYGIIHQQA ISVHGRNQ GPLDGSID DVGWRGVKD MEITTDNNG THTSANLL  
BAB15793 1 -----W HLFQWS--DG TGVLEBEGF SSTANETIE GKYGIIHQQA ISVHGRNQ GPLDGSID DVGWRGVKD NATTEDNNG THTSANLT  
CAB61358 1 -----VG  
CAB61827 1224 FFGTLCPCP GLGGV-S-G HGQCCDRPLG GGBE-HEGF HTANBEVEL GRGYNITGV IDAHGLQOE GLQDGSIV NVGWOGLRD QKITSPQPR KIDNANVQ  
BAA13377 967 FFGTLCPCP GLGGV-S-G HGQCCDRPLG GGBE-HEGF HTANBEVEL GRGYNITGV IDAHGLQOE GLQDGSIV NVGWOGLRD QKITSPQPR KIDNANVQ

175SHARE 313 DPGKASIK AAGFCNGTIV TAINAETS NGSSTKAL KRTTPGNRV VRKAGYTGID IVLEINPL ENHGGDRNA BTQTGPNQA VNLPLKYTG DG-KVSLIN  
BAB15793 90 NSDITASIK AAGFCNGTIV TAINAETS NGSSTKAL KRTTPGNRV VRKAGYTGID IVLEINPL ENHGGDRNA BTQTGPNQA ANPLPAYTG DG-KVTLIN  
CAB61358 3 EAVGTASIK AAGFCNGTIV TAINAETS NGSSTKAL KRTTPGNRV VRKAGYTGID IVLEINPL ENHGGDRNA BTQTGPNQA ANPLPAYTG DG-KVTLIN  
CAB61827 1433 DSAGASTIA AAGYSGNGIF SEVDPAHG HGGSPHAN TKVAPQRTI TQDGMGID ELQEINSL IHGGHHA BTPTGPOV SLSREGYSG DQRTIELD  
BAA13377 1076 DSAGASTIA AAGYSGNGIF SEVDPAHG HGGSPHAN TKVAPQRTI TQDGMGID ELQEINSL IHGGHHA BTPTGPOV SLSREGYSG DQRTIELD

175SHARE 422 VLTNNGGS PFAPNTEQ DQRIKPD Y-TGDGIVR GSIYGLPKN PSTSQYFFQL QEHAVRELAP PGPTVFAP- --LSSSFNHE PRKIDWQCG LMSQVRYHV  
BAB15793 199 VLTNNGGS EPAINHTQO VERTIKPN Y-IGDGPTR GSIYGLPKN PSTSQYFFQL QEHAVRELAP PGPTVFAP- --LSSSFNHE PRKIDWQCG LMSQVRYHV  
CAB61358 112 VLTNNGGS EPAINHTQO VERTIKPN Y-IGDGPTR GSIYGLPKN PSTSQYFFQL QEHAVRELAP PGPTVFAP- --LSSSFNHE PRKIDWQCG LMSQVRYHV  
AAF82398 1 -----MQVLRVHV  
CAB61827 1543 SKNNGGS PYATKSTGD QRTITDITA HTVGDGUTR ARVGLLIRD KHAS--FFSL RLLEYKELG DGPTTFVPH ADLMSNSQD ELARIAHRQ L--VFRVHV  
BAA13377 1186 SKNNGGS PYATKSTGD QRTITDITA HTVGDGUTR ARVGLLIRD KHAS--FFSL RLLEYKELG DGPTTFVPH ADLMSNSQD ELARIAHRQ L--VFRVHV

175SHARE 528 VGLQLLNL LKVTISATLL QGEPVSI SVS QDTVFIDNEA KVLSSDIIST NGVHVIDKL LSPKNLLITP KDALGRVLQN LTTVAANHGY TKFSKLQDS GLLSVITOSI  
BAB15793 305 VAHQLLLEN LKLSNATSL QGEPVSI SVS QSTVYDNKA KI ISSDIIST NGVHVIDKL LSPKNLLITP KINSGRILQN LTTLATNNGY IKFNSLIQDS GLLSVITDPI  
CAB61358 218 VAHQLLLEN LKLSNATSL QGEPVSI SVS QSTVYDNKA KI ISSDIIST NGVHVIDKL LSPKNLLITP KINSGRILQN LTTLATNNGY IKFNSLIQDS GLLSVITDPI  
AAF82398 10 VAHQLLLEN LKLSNATSL QGEPVSI SVS QSTVYDNKA KI ISSDIIST NGVHVIDKL LSPKNLLITP KINSGRILQN LTTLATNNGY IKFNSLIQDS GLLSVITDPI  
CAB61827 1648 VGRRLRSED LLEQYATALL SGHPLRFSEB GSGIYNDFA RVVSSDHEAV NGILHFIDRV LPPPEALHWE PDDAPIPRRN VTAAGQFGY KIFSLKLVA GLLELREAS  
BAA13377 1291 VGRRLRSED LLEQYATALL SGHPLRFSEB GSGIYNDFA RVVSSDHEAV NGILHFIDRV LPPPEALHWE PDDAPIPRRN VTAAGQFGY KIFSLKLVA GLLELREAS

175SHARE 638 HTPTVFWPT DKALZALPPE QODPLFNQDN KDKLSYLYK HVIRDSKALA SLPERSASMK TLQSSLSVR STGSDIGEL FLNQMRFI HRGLLFDXV AYGIDLLN  
BAB15793 415 HTPTVFWPT DQALHALPAE QODPLFNQDN KDKLKEYLYK HVIRDAKULA VDLPTSTAMK TLQSSLSVK GAGRDIGDL FLNQTRIV QRELLFDLXV AYGIDLLD  
CAB61358 328 HTPTVFWPT DQALHALPAE QODPLFNQDN KDKLKEYLYK HVIRDAKULA VDLPTSTAMK TLQSSLSVK GAGRDIGDL FLNQTRIV QRELLFDLXV AYGIDLLD  
AAF82398 120 HTPTVFWPT DQALHALPAE QODPLFNQDN KDKLKEYLYK HVIRDAKULA VDLPTSTAMK TLQSSLSVK GAGRDIGDL FLNQTRIV QRELLFDLXV AYGIDLLD  
CAB61827 1758 HRPFTHWPT DAAFRALPED RQWLYHEDH RDKLALILG HIRNVEALA SLDNLGLPLR TMGTPTISFS SRTRP-GEEL MVGEDDARIV QRLHFBGGL AYGIDQLLEP  
BAA13377 1401 HRPFTHWPT DAAFRALPED RQWLYHEDH RDKLALILG HIRNVEALA SLDNLGLPLR TMGTPTISFS SRTRP-GEEL MVGEDDARIV QRLHFBGGL AYGIDQLLEP

175SHARE 748 PTLOGRDTF TTFDIP-GE GSITPTKAP LKSKPKGVK K--LY- --NLPF R----- --RNVE-G QNTVTVIQT PRSHGYMP DQAGGGPD  
BAB15793 525 PTLOGRDTF TTFDAS-GE GSINTPSP RWSKPKGVK K--LY- --N-LPF K----- --RNLE-G RERSLVIOI PRSHGYMP DQAGGGPD  
CAB61358 438 PTLOGRDTF TTFDAS-GE GSINTPSP RWSKPKGVK K--LY- --N-LPF K----- --RNLE-G RERSLVIOI PRSHGYMP DQAGGGPD  
AAF82398 230 PTLOGRDTF TTFDAS-GE GSINTPSP RWSKPKGVK K--LY- --N-LPF K----- --RNLE-G RERSLVIOI PRSHGYMP DQAGGGPD  
CAB61827 1867 PGLGARDF ETPLRLNLI SI-SLEPP BSGQSGSFE AWRFPKFW TSPPLHSLG RSVVHPSLW GRPQGLRG HRMTVTWK PSFPHYGS DQAGGGPD  
BAA13377 1510 PGLGARDF ETPLRLNLI SI-SLEPP BSGQSGSFE AWRFPKFW TSPPLHSLG RSVVHPSLW GRPQGLRG HRMTVTWK PSFPHYGS DQAGGGPD

175SHARE 833 PTANNGMR DLYTMCQQL YTCFNGPA ELKHGRFG DOPRSESH GQDBEITGS GHLLEIGWT AASTDTFPAV FAVTEA SV HATKENNT VNLNVEBQD  
BAB15793 609 APANNGVL DQYSATGEK YTCFNGPA ELKHGRFG DOPRSESH GQDBEITGS GHLLEIGWT GQLEIGWT GPSDTQAVL PAVTTP SA HATKENNT ENLDBEBQD  
CAB61358 522 APANNGVL DQYSATGEK YTCFNGPA ELKHGRFG DOPRSESH GQDBEITGS GHLLEIGWT GPSDTQAVL PAVTTP SA HATKENNT ENLDBEBQD  
AAF82398 314 APANNGVL DQYSATGEK YTCFNGPA ELKHGRFG DOPRSESH GQDBEITGS GHLLEIGWT GPSDTQAVL PAVTTP SA HATKENNT ENLDBEBQD  
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BAA13377 1620 SPDRGVEM DQMSGQQL RSGFAGTA ELARGAPG HQACRIVH GRDEBLOGS GSPDRGWT GPEVQLEL QPVTPPAP EAVRAGNS ESLGVBQD

175SHARE 943 ITTVVDEK QNNG AKVA RSKQGTQVS ISKQKYGD GYSIEIDP ADGWNGHE HATKMTGP KHKEKSHY VGDGLN-EP EQLPIDRLQ INQGHADAX  
BAB15793 719 ITTVVDEK QNNG AKVA RSKQGTQVS ISKQKYGD GYSIEIDP ADGWNGHE HATKMTGP KHKEKSHY VGDGLN-EP EQLPIDRLQ INQGHADAX  
CAB61358 632 ITTVVDEK QNNG AKVA RSKQGTQVS ISKQKYGD GYSIEIDP ADGWNGHE HATKMTGP KHKEKSHY VGDGLN-EP EQLPIDRLQ INQGHADAX  
AAF82398 424 ITTVVDEK QNNG AKVA RSKQGTQVS ISKQKYGD GYSIEIDP ADGWNGHE HATKMTGP KHKEKSHY VGDGLN-EP EQLPIDRLQ INQGHADAX  
CAB61827 2087 RVTVADLQ DGHGG SEHA NSQVGMVT TILPDYEGD GWSRARNP TDGHRGSE HANLSTGLN TRREHAGY VGDGLN-LEE SEPPFDR LG QPPEHSDAM  
BAA13377 1730 RVTVADLQ DGHGG SEHA NSQVGMVT TILPDYEGD GWSRARNP TDGHRGSE HANLSTGLN TRREHAGY VGDGLN-LEE SEPPFDR LG QPPEHSDAM

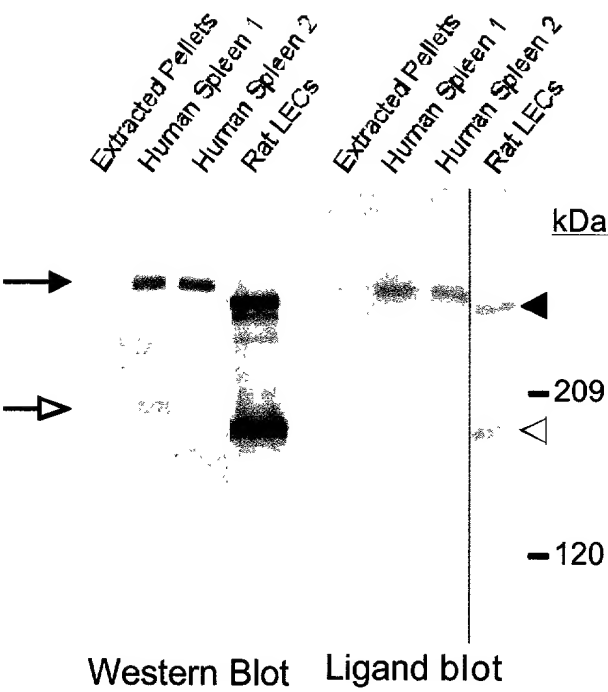
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BAB15793 741 VDLHFQDIT VGVFHLRSP GLYKLTFDKA REA ANEAAT MATYNQLSA QKAKYHLSA GWLETGRVAY PTAFASQNG SGVVGIVDYG PRANKSEMD VFRYMKDN  
CAB61358 533 VDLHFQDIT VGVFHLRSP GLYKLTFDKA REA ANEAAT MATYNQLSA QKAKYHLSA GWLETGRVAY PTAFASQNG SGVVGIVDYG PRANKSEMD VFRYMKDN  
AAF82398 2197 TDQHFQER AGVHLQATS GFYQINFSEA EAAEAGAV LASFPQLSAA QQLGPHILM GWLANGSTAH PVVFPVADG NGRVGVISLG ARNLSERWD AYFRVQDVA  
BAA13377 1840 VDLHFQER AGVHLQATS GFYQINFSEA EAAEAGAV LASFPQLSAA QQLGPHILM GWLANGSTAH PVVFPVADG NGRVGVISLG ARNLSERWD AYFRVQDVA

175SHARE 1162 ITKAGYVGD GFS-IGNLL QVLSMPSFLT NFLTEVLA FS KSSARGAPL KHLTDLISIRG TLFVPQNSGL GENETLSGRD IEHHLNVNM SPYNDLVNGT FLIRMLGSQD  
BAB15793 938 ITKAGYVGD GFS-IGNLL QVLSMPSFLT NFLTEVLA FS KSSARGAPL KHLTDLISIRG TLFVPQNSGL GENETLSGRD IEHHLNVNM SPYNDLVNGT FLIRMLGSQD  
CAB61358 849 ITKAGYVGD GFS-IGNLL QVLSMPSFLT NFLTEVLA FS KSSARGAPL KHLTDLISIRG TLFVPQNSGL GENETLSGRD IEHHLNVNM SPYNDLVNGT FLIRMLGSQD  
AAF82398 643 ITKAGYVGD GFS-IGNLL QVLSMPSFLT NFLTEVLA FS KSSARGAPL KHLTDLISIRG TLFVPQNSGL GENETLSGRD IEHHLNVNM SPYNDLVNGT FLIRMLGSQD  
CAB61827 2307 IRRNGFVG GISTNGKLL DVLAATANFS TFYGMLLGYA NATQRLDPL DFLDELTYK TLFVPVNEG VDNMTLSG PD LEHLASNATL LSN-ASQK LLAHSGSL  
BAA13377 1950 IRRNGFVG GISTNGKLL DVLAATANFS TFYGMLLGYA NATQRLDPL DFLDELTYK TLFVPVNEG VDNMTLSG PD LEHLASNATL LSN-ASQK LLAHSGSL

175SHARE 1271 LITFS--QD QLHQ-ETRFV DGRSILQWDI IAANGILHI SEPLRAPPA ATA---AHSG LGTIFCAV LVTGAIA--L AAYSYFRIR RTIG--FQHF DQKRLMSWL  
BAB15793 1047 LITAS--QD PLQPTETRFV DGRAILQWDI FASNGIHHV SRPLKAPPAP VTL---THIG LGAGIFFAI LVTGAVA--L AAYSYFRIR RTIG--FQHF ESEEDINVA  
CAB61358 924 LITAS--QD PLQPTETRFV DGRAILQWDI FASNGIHHV SRPLKAPPAP VTL---THIG LGAGIFFAI LVTGAVA--L AAYSYFRIR RTIG--FQHF ESEEDINVA  
AAF82398 752 LITAS--QD PLQPTETRFV DGRAILQWDI FASNGIHHV SRPLKAPPAP VTL---THIG LGAGIFFAI LVTGAVA--L AAYSYFRIR RTIG--FQHF ESEEDINVA  
CAB61827 2416 IISDAGPINS SWAPVAGTV VVSRIIWDI MAFNGIHAL ASPLLAPPQ QAVLAPEAP VAVG--GAV LAAGALLGLV AGALYLRAG KPMGPFPSAF QAEDDADDF  
BAA13377 2059 IISDAGPINS SWAPVAGTV VVSRIIWDI MAFNGIHAL ASPLLAPPQ QAVLAPEAP VAVG--GAV LAAGALLGLV AGALYLRAG KPMGPFPSAF QAEDDADDF

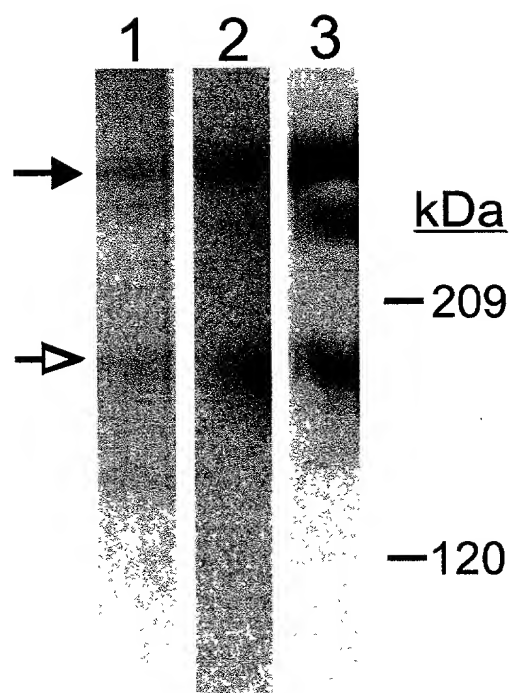
175SHARE 1370 LASSSP-RIS QTLQNRQRR HQSPPTUPS QTLNRIWRT ATLMHGCPD MRSQATVTV VFR  
BAB15793 1147 LKQOPENIS NFLY-ESTTS APPRPSYDF TDSER----- --QLEGNDF LRIL  
CAB61358 1024 LKQOPENIS NFLY-ESTTS APPRPSYDF TDSER----- --QLEGNDF LRIL  
AAF82398 852 LKQOPENIS NFLY-ESTTS APPRPSYDF TDSER----- --QLEGNDF LRIL  
CAB61827 2524 SPWQ-BSTN- PTLVSVNFV FGSDTFCFP ID----- -SLEEDFPD TQRLITVK-----  
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Figure 29





**Figure 3 0**



# Figure 31

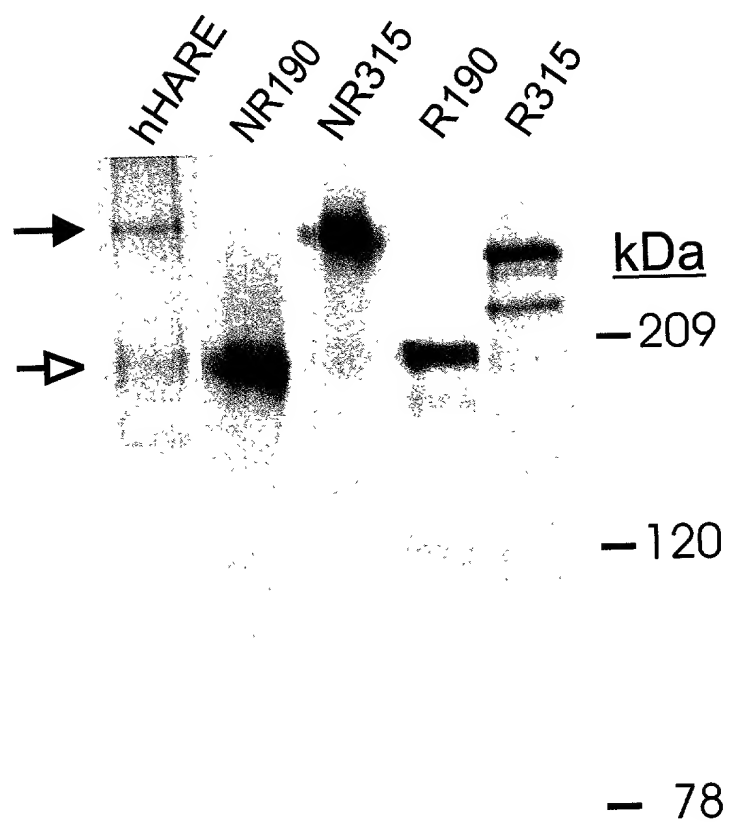
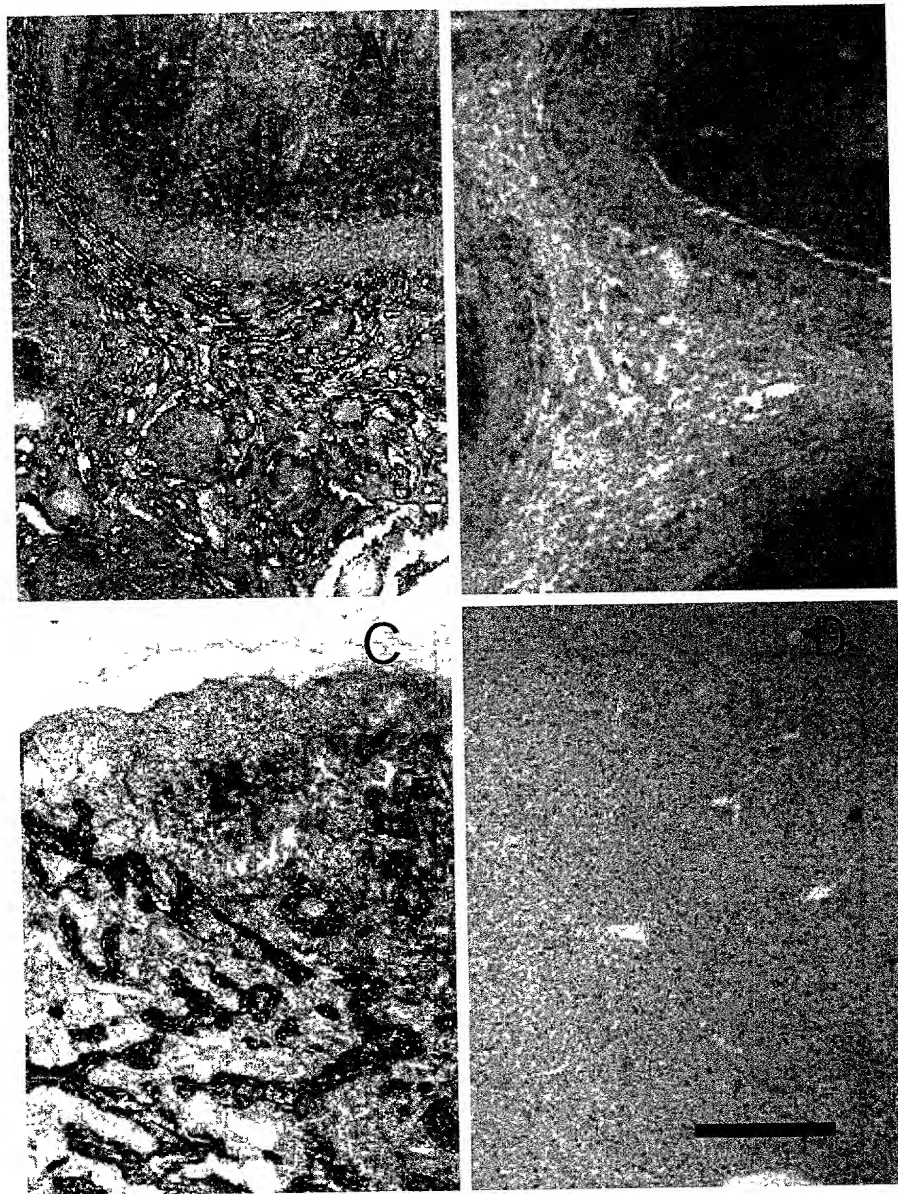


Figure 3 2



### Figure 33

1 ATTCATATAATCTGGCGAATGCAATCTGAGGCTCGCGATGCTACACAGTGTTCCTCCAAACAACATGCCATCGAGAAATACATCAGGAGAGAAAGTCTTGCTCTAGAGGAGGAC  
1 Q Y Q N L A N A I E A D A Y T V P A P N N N A I E N Y I R E K K L S L E E D

121 GTCCTCCGGTATCATGTGGTCTCGGAGGAGAACTCCTGAAGAATGACCTGCACATGGCATGCATGTGAGACATGCTGGGTTCTCTATTCTTACCTTCTTCTCCATATGAC  
41 V L R Y H V H V L E E K L L K N D L H N G M H N R E T M L G F S Y F L S F F L H N D

241 CAGCTCTATGTAAATGAGGCTCAATAAACTACCAACATGATGCCACTGATAGGAGATGTGATCCATGGCTTGGGAAATTCAGAGAACAGATGTGATAATAATGACACT  
81 Q L T Y V N E A P I N Y T N V A T D K G V I H G L G K V L E I Q K N R R C D N N D T

361 ACTATTATCAGGAGAGATGTAGACATGCTCTGAGCTGACCTGCCATCTCGGACTAAATCTCTAGTATGTAGAGAGAGGAGATGCATCTATACCTCTATTTCATGGGAAGACGA  
121 T I I R G R C R T C T S S E L T C P F G T K S L L G N E K R K C I Y T S Y F M G R

481 ACCCTGTTTATTGGTGCCAGCAAAATGTGTGAAGACCGCTCATACGAGAGATGCTGGCGGCTCTTTGGCCCAATGCCAGCCGCTGACCGAGATGCCAGAGATGCTGTGCTTT  
161 T L F I G C Q P K C V R T V I T R E C C A G F F G P Q C Q P C P G N A Q N V C F

601 GGTATGSCATCTGTTTGGATGGAGTGAATGCTGTGTGTGAGTGTGGGGAGGGCTTCAGSCGACAGCCTCGAGACGCTGACCGAGAGTACGGCATCCCTGTGACCAA  
201 G N G I C L D G V N G T G V T G E C E G E F S G T A C E T C T G G K Y I H C D Q

721 GCATGTCTTGTGTCATGGAGATGCAACCAAGGACCTTGGGAGATGGCTCTGTGATCTGTGCTTGGCTGGGAGAGTGCATGTGACATGCAACCAAGAGAACACTGCAAA  
241 A C S C V H G R C N Q G P L L G D G S C D C D V G W R G V H C D N A T T E D N C N

841 GGGACATGCCATACAGCGCCAATGCTCTACCAACTCAGATGGTACAGCTTATGCAAGTGTGCAGCAGGATTCGAAGGAAACGGGACCATCTGCACAGCAATCAATGCTGTGAGATC  
281 G T C H T S A N C L T N S D G T A S C K C A A G F Q G N G T I C T A I N A C E I

961 AGCAATGGAGGTGCTCTGCAAGGCTGACTGTAAAGAGAACCAACCCAGGAAGGAGTGTGCACGTGCAAGCAGGCTACAGGGTGTGATGGCATTTGTGTGCTGGAAATCAACCGGTGT  
321 S N G G C S A K A D C K R T T P G R R V C T C K A G Y C T G D G I V C L E I N P C

1081 TTGAGCAACCTGGTGGCTGTGACAAAGATGGCGAGTGCACACAGACCCACAGGCTGCCCTGAATCTTTGGCAGCATACCTGAGATGGAAGGCTGCCACATCATCAAT  
361 L E N H G G C D K N A E C T Q T G P N Q A A C N C L P A Y T G D G K V C T L I N

1201 GCTCTGTTAACTAAATATGGCGGCTGTAGTAGTATGTGCCATCTGCAACCACTGCGGCAAGTAGAAAGGACTTGTACTTGCAGCCAACTACATTGGAGATGGATTACCTGCCGGGG  
401 V C L T T K N G G C S E A F A I C N H T G Q V E R T C T C K F N I G D G F T C R G

1321 AGCATTTATCAGGAGCTTCCCAACACCCGAAAACTTCCAGTATTTCTTCCAGTTGCAAGGACTTCTGTAAGATCTGGTGGCCGAGCCCTTCACTGTTTTCGACCTTTATCT  
441 S I Y Q E L P K N P K T S Q Y F F Q L Q E H F V K D L V G P G P F T V F A P L S

1441 GCAAGCTTTGATGAGGAGCTCGGTTAAAGACTGGGACAAATACGGTTTAACTCCCGAGGTTCTTCGTACCATTTGTGTGCTGCGCTGCCACAGCTGCTTCTGGAAAGCTGAAATTTGATC  
481 A A F D E A R V K D W D K I Y G L H P Q V L R Y H V Y A C H Q L L E N L K L I

1561 TCAAAATGCTACTTCCCTCAAGGAGAGCCAAATGATCATCTCGGTCTCTCAGAGCAGCGGTATATAAACAATAGGCTAAGATCATATCCAGTGATCATCAGTACATTAATGGATGTT  
521 S N A T S L L Q G E P I V I S V S Q S T V Y I N N K A K I I S S D I I S T N G I V

1681 CATATCATAGACAAATGTCTATCTCCCAAAATTTGCTTATCACTCCCAAGACAACTCTGGAAGAATTTCTGCAAAATCTTACGACTTTGGCAACAAACAATGGCTACATCAAATTTAGC  
561 H I I D K L L S P K N L I T P K D N S G R I L Q N L T T L A T N N G Y I K F S

1801 AACTTAATCAGGACTCAGGTTTGTGAGTGTCTACACGATCCATCCATCAGCCAGCTCACTCTTCTGGCCACGACCAAGCCCTTCATGCCCTACTGCTGAACACAGGACTTC  
601 N L I Q D S G L L S V I T D P I H T P V T L T F W P T D Q A L H A L P A E Q O D F

1921 CTGTTCAACCAAGACAAAGGACAGCTGAAGGAGTATTTGAATTTTCACTTACAGGATGCAAGGTTTAACTGTGATCTTCCACATCCATCGCTGGAAGCTCCCTGGAAGG  
641 L F N Q D N K D K L K E Y L K F H V I R D A K V L A V D L P T S T A W K I T L Q G

2041 TCAGAGCTGAGTGTGAATTTGGAGCTGACGAGGACATCGGTGACCTTTCTGATGCTGGCAAACTGCAGAAATTTGGCAGCGGAGCTTGTGTTGACCTGGGTGSGCTACCGAT  
681 S E L S V K I G A G R D I G D C L F L N G O T C R I V Q R E L F D L G V A Y G I

2161 GACTGCTCTGATGTATGCCACCTCGGGGGCGCTGTGACACCTTTACTACTTTCGATGCTCGGGGAGTGTGGGAGCTGTGTCAATCTCCAGCTGCCAAGGTGAGTAAACCA  
721 D C L L I D A P T T L G G R C D T F T T F D A S G E C G C S C V N T P S C P R N S K P

2281 AAGCTGTGAAGCAAGTGTCTCTACAGCTGCTCCCTCAAGAGGAACCTGGAAGGCTGCGGGAGCGGTGACGCTGTGTGATACATCCCAAGGTGTGCAAGCTGCTCAAGCTGCTCTGCA  
761 K G V K Q K C L Y N L P F K R N L E G C R E R C S L V I Q I P R C C K I G Y F G R

2401 GACTGTACAGGCTGCCCTGGAGGACAGATGCCCGGTGATAATACCGGGGTGTCTGCTGTATCAGTACTCGGCCACCGGAGAGTGTAAATGCAACACCGGCTTCAATGGGACGGCGT  
801 D C Q A C G T G P G F D A P C N N R G V C L D Q Y S A T G E C K N T G F N G T A T

2521 GAGATGTCTGCGCGGGAGATTTGGCGCTGATGTCTGCGCTGTGCTCTCAGACAGGACATGCGATATGCGATCAGCGGCTCGCGGAGCTGCTTGTGAAACCGGGTGGACA  
841 E M C V R R F G P D C L P C G C S D H G Q C D D G I T G S G Q C L C E T G W T

2641 GGCCCCCTGCTGTGACACTCAGGCAGTTTTCCTGCGACTGTGTACGCTCTCTGTTCTGCTCATGCCACTGTAAAGAGAGAACAAACGCTGTGAGTGTAACTGGATTATGAAGATGACGGA  
881 G P S C D T Q A V L P A V C T P P C S A H A T C K E N N T C E C N L D Y E G D G

2761 ATCATCTCAGATTTGTGATTTCTGCAACAGGACCAAGGGGCTGTGCAAAAGGTGGCCAGATGCTCCAGAAAGGCGACGAAGGTCTCTGTGAGCTGCGCAGAGGATACAAAGGGGAC  
921 I T A T C T V V D F T C T C K Q A G G C A D N G S C A K A V A R C S Q K A T K V S C S C Q K Y I R G D

2881 GGGCAGCAGCTGCACAGATAGACCCCTGTGCGACAGCGCTTAAACGAGGGGTGTACAGGACGCCACTGTAAAGATGACAGGCGCGGCGAAGCAAGTGTGAGTGTAAAGTCACTAT  
961 G H S C T E I D P C A D G L N G G C H E H A T C K M T G P G K H K C E C K S H Y

3001 CTGCGAGATGGGCTGAATCTGAGCGGAGACGCTGCCATGACCGCTGTCTACAGCAATGGGAGTGGCATGCAAGCGCCAAATGTGTGCACTTCCATCTCAGGATACCACTGTT  
1001 V G D G L N C E P E Q L F I D R C L Q D N G A G G C C H A D A K C V D L H F Q D T T V

3121 GGGGTGTTCATCTACGCTTCCCACTGGGCGAGTAAAGCTGACCTTTGACAAACCGAGAGGCTGTGCAAGGACGCTGCGACATGGCACTTCAACAGCCTCTCTATGCCAG  
1041 G V P H L R S P L G Q Y K L T F D K A R I E A C A N E A A T M A T Y N Q L S Y A Q

3241 AAGCGCAAGTACCCACTGTGCTCAGCAGCTGCTGGAGACGGGCGGGTGTGCTTACCTCCAGCCTCTGCGCTCCAGAACTGTGGCTCTGCTGTGGTATGGGATGTGATGACCT  
1081 K A K Y H L C S A G N L E T G R V A Y T P A F A S Q N C G S G V Y G I V D Y G P

3361 AGACCCAAACAGAGTGAATGTGGGATGCTCTGCTATCGGATGAAGATGTGAATCTCACTGCAAGGTGGGCTGTGTGGAGATGGCTTCTATGAGTGGGAACCTGTCTGACAGTC  
1121 R P N K S E M W D V F C Y R M K D V N C T C K V G Y V D G F S C S G N L L Q V

3481 CTGATGCTCTTCCCTCACTACAACTCTCTGACGGAAGTGTGCGCTATTCCACAGCTCAGCTCGAGGCGGTGCAATTTAGAAACCTGACTGACTTGTCCATCCGCGGACCTCT  
1161 L M S F P S L T N F L T E V L A Y S N S S A R G R A F L E H L T D L S I R G T L

3601 TTGTGGCCAGAGACGATGGGCTGGGAGCAATGAGACCTTGTCTGGCGGGAATCGAGCACCCTCGCAATGTGACATGTTTCTTCAATGACCTTGTCAATGGCAACCTCT  
1201 F V P Q N S G L G E N E T L T S G R D I E H L L A V S M F F Y N D L V N G T L

3721 CAAACAGGCTGGGAAGCAGCTGCTCATCTGCGAGCGACCCATCCAAACCGAGAGACAGGTTTGTATGGAGAGCCATTCTGCAAGGACATCTTTCGCTCCATAGGG  
1241 Q T R L G S K L L I T A S Q A D D P L Q P T E T R F V D G R A I L Q W D I F A S N G

3841 ATCATTCATGTCAATTCAGGCTTTAAAGACCCCTGCGCCCGTGACCTTGACCCACACTGGCTGGGAGCGGATCTCTTTGCCATCATCTGTGTGACTGGGGCTGTGCTCTG  
1281 I H I V I S R P L K A P A P A V T L T H T G L G A G I F F A I I L V T G A V A L

3961 GCTGCTTACTCTCTATTCGATAAACCCGAGAACATCGGCTTCAGCATTTTGAATCGGAAGGACATTAATGTGACCTTCTGGCAAGCAGCCTGAGATATTCGAACCCC  
1321 A A Y S Y F R I N R R T I G F Q H F E S E E D I N V A A L G K Q Q P E N I S N P

4081 TTGATGTAGAGCAACCTCAGCTCCCCAGAACCTTCTACGACCCCTTCACGGACTGGAAGAACCGGAGCTTGAGGGCAATGACCCCTTGAGGACCTGTGAGGCGCTGGAGCGGAG  
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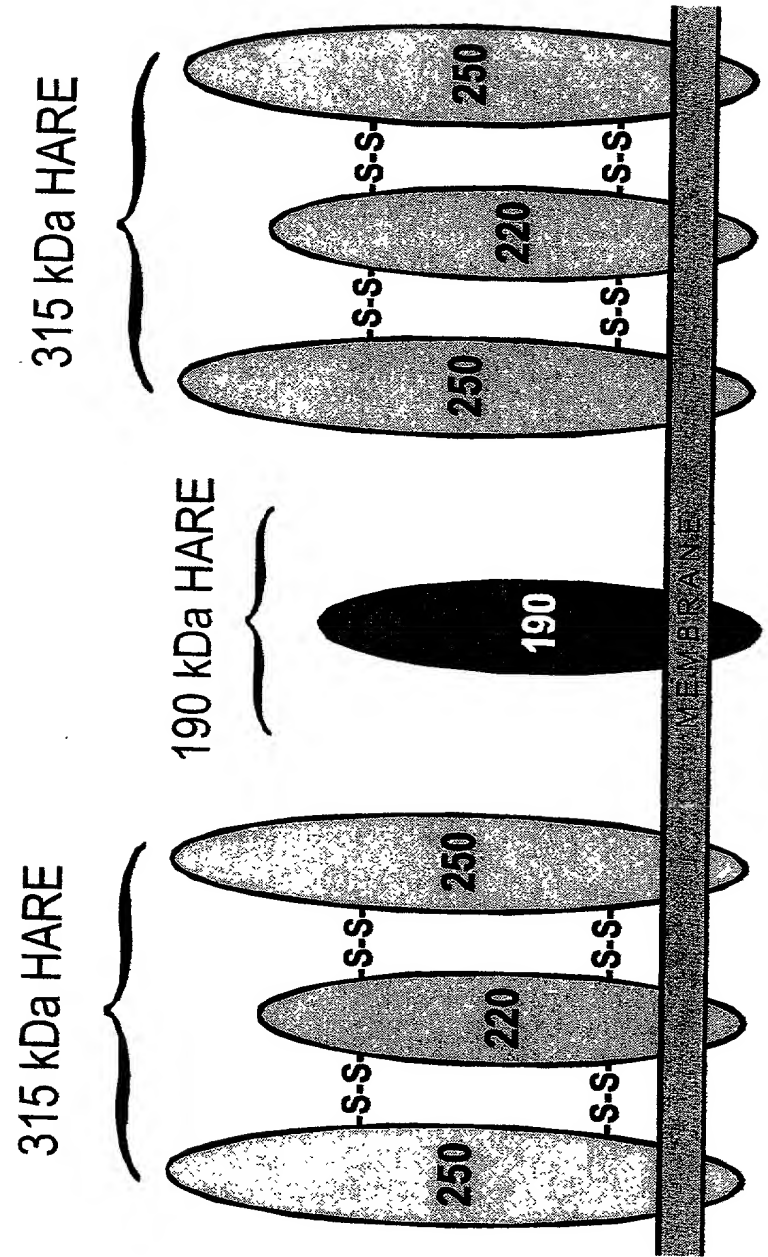
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Figure 35

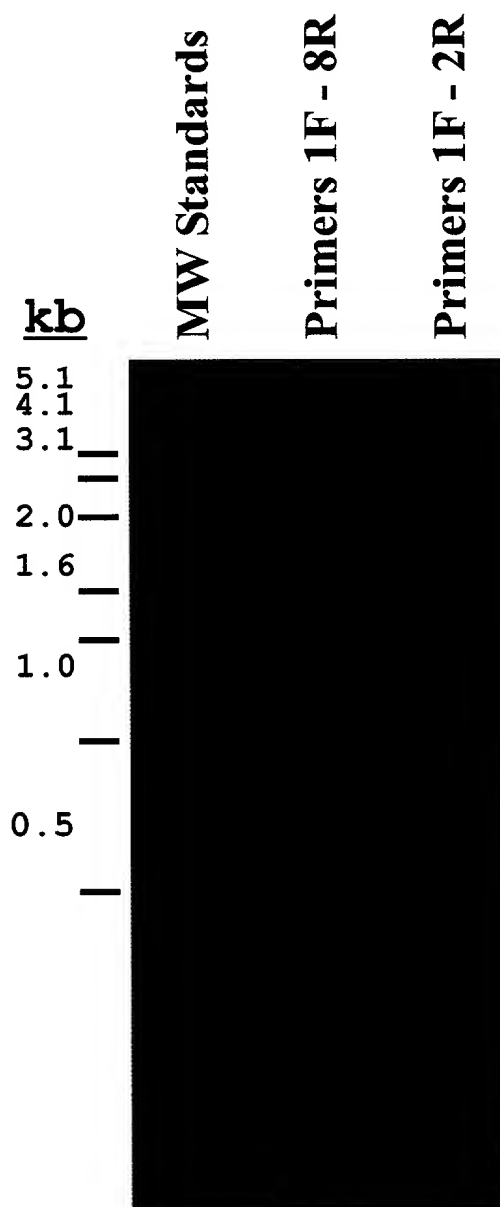
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rHARE 23 IHYNLASATESADAYTVFVP NNEAIENYIREKATSLKED ILRHHVVLGEKLLKNDLHNG MHRETMLGFSYLLAFLRLND QLYVNEAPINYNVATDKGV  
hHARE 101 IHGLGKVLBIQKNN DNDTA TIIRGR RT ISSELT PFGT KSLGNEKRR IYTSYFMGR TLFIG QPK VRTVITRE C AGFFGPOCQPCPGNAQNVCF  
rHARE 123 IHGLEKVLBIQKNN DNDTA IIVRGE GK SQAP PLET IIVRGE GK SQAP PLET KPL-RETRK IYTSYFMGR SVFIG QPK VRTIITRA W LASLAHNAKPAPGEVKMCAL  
hHARE 201 GNGICLDGVNGTGV E GEG FSGTA ET TEGKYGIH DQ A S V HGR NOGPLDGS D DVGWRGVH DNATETDN N G HTSAN LTNSDGTAS K  
rHARE 222 GTASVWDGVNGTGV O GLG FNGTA ET TEGKYGIH DQ A S V HGR SOGPLDGS D DVGWRGVH DMEITTDN N G HTSAN LLDPDGKAS K  
hHARE 301 AAGFQNGT I TAINA EI SNGG SAKAD KRTTPGRV T KAGYTG DGIV LEINP LENHGG DNAB TOTGPNQ AAN LPAYTGDGKV TLIN  
rHARE 322 AAGFRNGT I TAINA ET SNGG STKAD KRTTPGNRV V KAGYTG DGIV LEINP LENHGG DRNAE TOTGPNQ AVN LPAYTGDGKV SLIN  
hHARE 401 VLTNNGG SEFAI NNN Q VERT T KPNYIGDFT RG SIYQELPKNPKTSQYFFOLQ EHFVKDLVGPPTVFAPLS AAFDEEARVKDWDKYGLMPQ  
rHARE 422 VLTNNGG SPFAF NNN Q DQRI T KPDYTG DGIV RG SIYGELPKNPSTSQYFFOLQ EHAVERLAGPGPTVFAPLS SSFNHEPRKDWDOQGLMSQ  
hHARE 501 VLRHVVA HOLLLENKLI SNATSLQGEPIVTSVSQSTV YINNKA K I SSDIISTNGIV HIIDKLLSPKNLLITPKDMS GRILQNTLTATNNGYIKPS  
rHARE 522 VLRHVVG QOLLLENKVT TSATTLQGEFVSISVSQSTV FINNEAKV SSDIISTNGIV HVIDKLLSPKNLLITPKDAL GRVLQNTLTATVAANHGYTKPS  
hHARE 601 NLIQDSGLLSVITDPIHTPV TLFWPTDQALHALPAEQQDF LFNQDNKDKLKEYLKHFHVR DAKVLAVDLPTSTAWKTLOG SELSVK GAGRDIGDLFLNG  
rHARE 622 KLIQDSGLLSVITDSIHTPV TVFWPTDKALEALPPEQQDF LFNQDNKDKLKEYLKHFHVR DSKALASDLPRSASWKTLOG SELSVR GTGSDIGELFLNE  
hHARE 701 QTRIVQRELLFDLGAVYGI D LLLIDPTLGGRTDTFTTFD ASGE GS VNTPS PRWSKP KGVKQK LYN-LPFKRNLEG RER SLVLIQIPR KGYFG  
rHARE 722 QMRFIHRGILLFDVGAVYGI D LLMNPTLGGRTDTFTTFD IPGE GS IFTPK PLKSKP KGVKKR IYNPLPFRNVEG QNL TVVIQTPT KHYFPM  
hHARE 800 RDQA PGGPDAP NNRGM LDQYSATGE KNTGFNGA EM WPGREGPD LPCG SD HGQ DDGITGSGO L ETGW TGPS DTQAVLPV TTP S  
rHARE 822 PDQA PGGPDTP NNRGM RDLYTPMGQ L HTGFNGA EL WHGRFGPD QPRS SE HGQ DEGITGSGE L ETGW TAAS DTPTAVFAV TPA S  
hHARE 900 AHAT KENNT E NLDYEGD GIT TVVDF KQNGG AKV AR SQKGTQVS S QKGYKG DGHS TEIDP ADGLNGG H EHAT KMTGPGKHK E KSH  
rHARE 922 VHAT TENNT V NLNYEGD GIT TVVDF KQNGG AKV AK SQKGTQVS S KKGKYG DGYS IEIDP ADGVNGG H EHAT RMTGPGKHK E KSH  
hHAR 1000 YVGDGLN EPEQLPIDR LQ DNGQ HADAK VDLHFQDIT VGVFHLRSPGLQYKLTFDKA REA ANEAATMATYNQLSYA QKAKYHL SAGWLETGRVAY  
rHARE 1022 YVGDGVD EPEQLPLDR LQ DNGQ HPDAS ADLYFQDIT VGVFHLRSPGLQYKLTFDKA KEA AKEAATATATYNQLSYA QKAKYHL SAGWLESGRVAY  
hHARE 1100 PTAFASQNGSGVVGIVDYG PRPKSEMWDVFTYRMKDVN A KGVYVGDFGS SGNLLQ VLMSFPSTNFLTTEVLAYSN SSARGRAFLHLLTDL SIRGT  
rHARE 1122 PTTVASQK GANVVGIVDYG SRANKSEMWDVF YRMKDVN A KGVYVGDFGS SGNLLQ VLMSFPSTNFLTTEVLAFSK SSARGQAFLLKHLTDL SIRGT  
hHARE 1200 LFVPQNSGLGENETLSGRDI EHLLANVSMFFYNLDLVNGT LQTRLGSKLLITASQDPLQ LQTRFVDRGAILQWDIFASN GIITHVISRPLKAPPAPVTLT  
rHARE 1222 LFVPQNSGLPGNKLSGRDI EHLHTNVNVFFYNLDLVNGT LRTMLGSQLLITFSQDQLHQ -ETRFVDRSILQWDIIAAN GILHI ISEPLRAPPTAATAA  
hHARE 1300 HTGLGAGIFFAIIILVTGAVA LAANSYFRINRRRTICFOHFE SEED INVAALGKOOPENISN PTEST SAPPEPS DPTTD SEERQLEGN DPLRTL  
rHARE 1321 HSGLGTGIFCAVVENTGAIA LAANSYFRINRRRTICFOHFE OKRTLSMWLLASSSPRISQT LCMRPQRHHPQSPVTPSQT LENRIWRATLWGHCGGPDMR  
rHARE 1421 SQATTVTVPR

Figure 36



# Figure 37

Amplification of the 1394 amino acid HARE  
Open Reading Frame from a human lymph  
node cDNA Library





# Figure 38

Schematic Organization of the Human HARE Gene on Chromosome 12  
(encoding 1357 of the 1394 amino acids disclosed here)

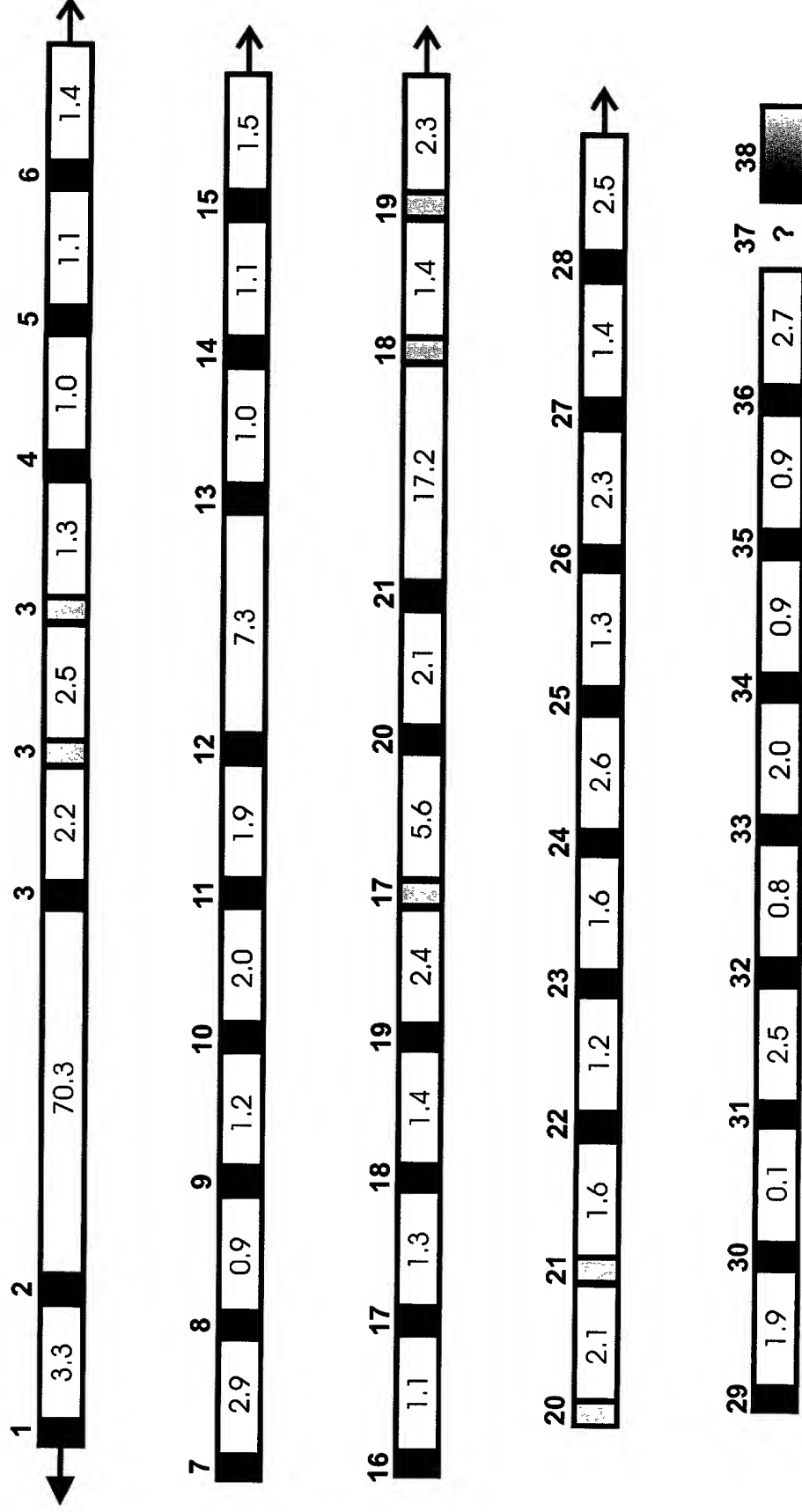


Figure 3 9

